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AAH70670
AAH70670;
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Matches
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WEDLINE=2288257; PubMed=12477932;

WEDLINE=2388257; PubMed=12477932;

WEDLINE=2388257; PubMed=12477932;

Alsaner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Alschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
Alschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
A blackhoko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A blackhoko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A blackhoko L., Marusina M., Poenivuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bromstein M.J., Usdin T.B., Garcia A.M., Gay L.J., Hulyk S.W.,
A Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Krzywinski M.I., Skalska U., Samilus D.E., Schnerch A., Schein J.E.,
A Jones S.J., Marra M.A.,
A Jones M.A., Butterfield Y.S.,
A Jones A.J., Marra M.A.,
A Jones M.A., Butterfield Y.S.,
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                                                                                                                                                          Gaps
375 375 Phosphothreonine (by CK2) (in vitro). 379 379 Phosphoserine (by CK2) (in vitro). 493 AA, 55111 MW, 9694CD302BEBBEDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                       DB 1; Length 493; 0.02;
                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S., Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
BMB.; BC070670; AAH-0670.1;
InterPro; IPR008253; Marvel.
InterPro; IPR010844; Occludin.
InterPro; IPR010844; Occludin.
EnterPro; IPR010844; Occludin.
Pfam; PF01284; MARVEL; 1.
Pfam; PF07303; Occludin. ELL; 1.
SEQUENCE 497 AA; 56202 MW; 269431E14ECDOEA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                 Query Match
60.3%; Score 79; DB
Best Local Similarity 58.3%; Pred. No. 0.02
Matches 14; Conservative 5; Mismatches
                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
                                                                                                                                                                                                      3 REESEEYMAAADEYNRLKOVKOPA 26
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                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGC82312 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
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MOD_RES
SEQUENCE
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RX MISSUE-Kidney,

RX Altasberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rtausner R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,

Ratschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rab S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Raba S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Rale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Ratesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rationez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative ".
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   Length 497;
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                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070670; AAH70670.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                         13-MAY-2004 (TrEMBLrel. 27, Created)
13-MAY-2004 (TrEMBLrel. 27, Last sequence update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sci. U.S.A. 99:16899-16903(2002).
Score 64; DB 2;
Pred. No. 2.5;
                                Pred. No. 2.5;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                            497 AA
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4; Mismatches
                                                                                                                                                             || | : :| ||||||| :|:
441 GLTEGTTQYQGVDDEYNRLKDLKR 464
                                                                                                                          1 GLREESEEYMAAADEYNRLKOVKO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GLREESEEYMAAADEYNRLKQVKQ 24
                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus; Xenopus.
   ch 48.9%;
1 Similarity 50.0%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dev. Dyn. 225:384-391(2002)
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                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                           with 20-1.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SUBCELLULAR LOCATION: Localized at tight junctions of both epithelial and endothelial cells. Highly expressed in lung and liver. Expressed at a lower level in brain.

-!- DOMAIN: The C-terminal is cytoplasmic and is important for interaction with 20-1. Necessary for the tight junction localization. Involved in the regulation of the permeability barrier function of the tight junction. The second extracellular domain may also be implicated in the permeability barrier function of the tight junction. The second extracellular domain may also be implicated in the permeability barrier function of the tight junction.
                                                                                                                                                                                                                                                                         IISSUE=Embryonic Drain;
MEDLINE=94103332; PubMed=8276896;
Furuse M., Hirase T., Itoh M., Nagafuchi A., Yonemura S., Tsukita S.,
                                                                                                                                                                Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                           J. Cell Biol. 123:1777-1788(1993).
-!- FUNCTION: May play a role in the formation and regulation of the tight junction (TJ) paracellular permeability barrier. Interacts
                                                                                                                                                                                                                                                                                                                                 "Occludin: a novel integral membrane protein localizing at tight junctions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Tight junction; Transmembrane. 1 57 Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic (Potential).
Potential.
Extracellular (Potential).
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AD0352A45A0231FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: Phosphorylated (By similarity).
SIMILARITY: Belongs to the ELL / occludin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
Cytoplasmic (Potential).
TYR/GLY-RICH.
                                                                (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 44, Last annotation update)
                               504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IntAct, Q91049; -.
InterPro; IPR008253; Marvel.
InterPro; IPR002958; Occludin.
InterPro; IPR010844; Occludin_ELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRULUSA:
Pfam; PF01284; MARVEL; 1.
Pfam; PF07303; Occludin ELL; 1.
PTAME; PR01258; OCCLUDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55863 MW;
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                                STANDARD;
                                                                                                                                                     Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A49467; A49467.
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                               091049;
15-DEC-1998 (
15-DEC-1998 (
05-JUL-2004 (
                                                                                                                                                                                                                                                                                                                            Bukita S.;
                                OCLN CHICK
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TRANSMEM
DOMAIN
                                                                                                                                     Name=OCLN;
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DOMAIN
TRANSMEM
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TRANSMEM
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SEQUENCE
                                                                                                                      Occludin
                OCEN_CHICK
RESULT 15
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Gaps
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Query Match
Best Local Similarity 43.5%; Pred. No. 13;
Matches 10; Conservative 7; Mismatches 6; Indels
                                                                                               : |:| :| :| |:| | : | 49 ITEDSPQYQDVAEEYNQLKDLKR 471
                                                                            2 LREESEEYMAAADEYNRIKOVKO 24
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Search completed: November 10, 2004, 12:27:22 Job time : 30.4475 secs

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Sequence 21, Appli
Sequence 4, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 146, Appli
Sequence 3218, Appli
Sequence 25685, A
Sequence 226, Appli
Sequence 236, Appli
Sequence 236, Appli
Sequence 236, Appli
Sequence 67, Appli
Sequence 7, Appli
Sequence 3287, Appli
Sequence 2387, Appli
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23238, A
23238, A
17844, A
2, Appli
19, Appli
25672, A
17670, A
17670, A
3563, A
                                                                                           ; Search time 19.9552 Seconds (without alignments) 222.664 Million cell updates/sec
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330
1 KGIISRLMSVEBELKRDHAE......ARLMSALTPAXRYVXHCXPL
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-294-298A-6

US-09-294-298A-6

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US-09-679-279-14

US-09-679-279-14

US-09-679-279-14

US-09-52-991A-32193

US-09-125-991A-32193

US-09-125-991A-32685

US-09-125-991A-32685

US-09-126-1285-1285

US-09-128-1285

US-09-128-1285
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                                                                                                                                                                                                                                                                         478139 segs, 66318000 residues
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                                                                                               November 10, 2004, 11:41:17
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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                                                              OM protein
                                                                                                                                                                                              Sequence:
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No.
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Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence 21202, A Sequence 20018, App Sequence 20018, A Sequence 32257, A Sequence 28883, A Sequence 14, Appli Sequence 4, Appli Sequence 19101, A Sequence 19101, A Sequence 28988, A Sequence 28988, A Sequence 22988, A Sequence 27, Appl Sequence 21647, A Sequence 21647, A Sequence 21647, A	ECULES AND USES THEREOF	Length 1135; ; Indels 0; Gaps 0;	MOLECULES AND USES THEREOF
4 US-09-252-991A-21202 4 US-09-198-452A-186 4 US-09-252-991A-320573 4 US-09-252-991A-320573 4 US-09-252-991A-320573 4 US-09-252-991A-128383 4 US-09-248-796A-128383 5 US-09-248-796A-18060 5 US-09-252-991A-18060 5 US-09-252-991A-28988 5 US-09-252-991A-28988 6 US-09-252-991A-28988 7 US-09-252-991A-28988 7 US-09-252-991A-28988 7 US-09-252-991A-28988	ALIGNMENTS 109294298A L. TRANSDUCING SYNAPTIC MOLECULES 105/09/294,298A 104-19 10/082,690 10/082,717 23 24 Lion of Unknown Organism: mamm	oore 72; DB 4; red. No. 0.26; Mismatches 5 21 1107	298A SDUCING SYNAPTIC 39/294,298A 2,690
54 16.4 389 .5 16.2 1111 .5 16.2 1111 53 16.1 124 53 16.1 124 .5 15.9 292 .5 15.9 527 .5 15.9 461 .5 15.6 107 .5 15.6 107 .5 15.6 15.5	ion US/ EHAE EHAE SIGNAL SIGNAL SIGNAL SIGNAL WABER: 6 998-04- 898-04- 1: 24 er: 2.1 rganism	imilarity 71.4; Conservative KGIISRLMSVEEEIKR	RESULT 2 US-09-294-298A-6 1 Sequence 6, Application US/09294; Patent No. 6723838 2 GENERAL INFORMATION: APPLICANT: HUGANIK, RICHARD L. APPLICANT: KIM, GJEHAE TITLE OF INVENTION: SIGNAL TRANS FILE REFERENCE: 48235/1699 CURRENT APPLICATION NUMBER: US/05/05/05/05/05/05/05/05/05/05/05/05/05/
2 2 8 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	RESULT 1 US-09-294-298A-21 Sequence 21, Applicat Fatent No. 672838 GENERAL INFORMATION: APPLICANT: HUGANIR, APPLICANT: HUGANIR, FILE PETERENCE: 4823 CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION CURRENT FILING DATE: 1 PRIOR APPLICATION NU PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 NUMBER OF SEQ ID NOS SOFTWARE: PATENTION NU SEQ ID NO 21 LENGTH: 1135 TYPE: PRT CRGANISM: UNKNOWN OF FEATURE: COTHER INFORMATION: COTHER INFORMATION: COTHER INFORMATION: COTHER INFORMATION:	Query Match Best Local S Matches 15 Qy 1	RESULT 2 US-09-294-296 Sequence 6, Patent No. GRAPERAL INF TILE APPLICANT: TILE OF I FILE REFER CURRENT FI PRIOR APPL PRIOR FILLI PRIOR FILLI

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TYPE: PRT CORGANISM: Homo sapiens US-09-621-976-4246
    LENGTH: 1423
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LENGTH: 356
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APPLICANT: HUGANIK, RICHARD L.
APPLICANT: HUGANIK, RICHARD L.
APPLICANT: HUGANIK, RUM GJEEHAE
TITLE OF INVENTION: SIGNAL TRANSDUCING SYNAPTIC MOLECULES AND USES THEREOF
FILE REFERENCE: 48238/1699
CURRENT APPLICATION NUMBER: US/09/294,298A
CURRENT FILING DATE: 1999-04-19
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1998-04-22
NUMBER OF SEQ ID NOS: 24
SOFTHARE: Patentin Ver: 2.1
SEQ ID NO 4
LENGTH: 1376
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APPLICANT: HUGANIR, RICHARD L.
APPLICANT: HUGANIR, RICHARD L.
APPLICANT: HUGANIR, RICHARD L.
APPLICANT: KIM, GUEERBE
APPLICANT: KIM, GUEERBE
CUERBIN GENERAL TRANSDUCING SYNAPTIC MOLECULES AND USES THEREOF
FILE REFERENCE: 48235/1699
CURRENT FILING NUMBER: US/09/294,298A
CURRENT FILING DATE: 1999-04-19
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHIN VOE: 2.1
SEQ ID NO 2
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                                                                                                                                        FEATURE: OTHER INFORMATION: Description of Unknown Organism: mammalian CTHER INFORMATION: SYNGAP-C US-09-294-298A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Unknown Organism: mammalian ; OTHER INFORMATION: SYNGAP-B US-09-294-298A-4
                                                                                                                                                                                                                                                      Query Match 21.8%; Score 72; DB 4; Length 1325; Best Local Similarity 71.4%; Pred. No. 0.31; Matches 15; Conservative 1; Mismatches 5; Indels
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21.8%; Score 72; DB 4; Length 1376;
Best Local Similarity 71.4%; Pred. No. 0.33;
Matches 15; Conservative 1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09294298A Patent No. 6723838
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Sequence 2, Application US/09294298A
Patent No. 6723838
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 1325
                                                                                       TYPE: PRT
ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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US-09-294-298A-4
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1 KGIISRLMSVEE-----SLKRDHAEMQAGCGLQTEDHLMPRRSAFA----SLDAVN 47
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                                                 FEATURE:
OTHER INFORMATION: Description of Unknown Organism: mammalian
CTHER INFORMATION: SYNGAP-A
US-09-294-298A-2
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1 Similarity 71.4%; Pred. No. 0.35;
15; Conservative 1; Mismatches 5; Indels
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APPLICANT: Wobert
APPLICANT: Wolchegursky, Yanina
APPLICANT: Wolchegursky, Yanina
TITLE OF INVENTION: Recombinant Megalomicin Biosynthetic
TITLE OF INVENTION: Genes and Uses Thereof
TITLE OF INVENTION: Genes and Uses Thereof
TITLE OF INVENTION: Genes and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/679,279
CURRENT FILING DATE: 12000-10-04
PRIOR APPLICATION NUMBER: US 60/159,024
PRIOR APPLICATION NUMBER: US 60/190,024
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1900-03-17
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASTESQ for Windows Version 4.0
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4246
LENGTH: 124
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18.9%; Score 62.5; DB
Best Local Similarity 31.8%; Pred. No. 27;
Matches 27; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                     1 KGIISRLMSVEEELKRDHAEM 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-679-279-14
; Sequence 14, Application US/09679279
; Patent No. 6524841
TYPE: PRT
ORGANISM: Unknown Organism
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US-09-621-976-4246
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Sequence 7681, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7681
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                                                                                          DB 3; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.6%; Score 58; DB 3 Best Local Similarity 26.5%; Pred. No. 8.9; Matches 18; Conservative 11; Mismatches
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17.6%; Score 58; DB 4
Best Local Similarity 44.0%; Pred. No. 9.5;
Matches 11; Conservative 6; Mismatches
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-7681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens
US-09-019-095A-24
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359 AGGDA 363
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| Sequence 25665, Application US/09252991A |
| Patent No. 6551795 |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: ARRUGINGAR FOR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: ARRUGINGAR FOR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: NUMBER: US 60/074,788 |
| PRIOR PELICATION NUMBER: US 60/074,788 |
| PRIOR PLICATION NUMBER: US 60/074,788 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-02-27 |
| NUMBER OF SEQ ID NOS: 33142 |
| LINGTH: 688 |
| LING
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Sequence 32193, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/094,788

PRIOR APPLICATION WUMBER: US 60/074,788

PRIOR APPLICATION WUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32193

LENGTH: 596
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                                                                                       Gaps
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                      Score 62; DB 4; Length 124;
Pred. No. 0.38;
3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 596;
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                                                                                                                                              6 RLMSVEBELKRDHAEMQAGCGLQTEDHLMPRRS 38
                                                                                                                                                                                                         32 RLVVLEKELLRDHLEMSROCHALQED--MOTRS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60; DB 4
Pred. No. 5.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT CORGANISM: Pseudomonas aeruginosa US-09-252-991A-32193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                      Query Match
Best Local Similarity 48.5%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35.1%;
Matches 13; Conservative
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Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ASLDA 45
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                                                                                                                                                                                                                                                                                                                                 -09-252-991A-32193
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NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: variable or unknown amino acid
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                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: (0)...(0)
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Persea sp.
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US-09-198-452A-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                        FEATURE:
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GENERAL INFORMATION:
APPLICANT: GENTY L. BEECON Et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
ENGRENT: 260
LENGTH: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BATRAD, YANNICK
APPLICANT: ROBINEAU, TIEURCE
APPLICANT: DIRECT, FRANCIS
APPLICANT: DIRECT, FRANCIS
APPLICANT: DIRECT, DANIELE
APPLICANT: DIRECT, DIRECT, DOINGE, DAPPLICANT: DIRECT, DOINGE, TITLE OF INVENTION: POLIUTANTS AND FOR APPLICATION OF ENVIRONMENTAL
TITLE OF INVENTION: POLUTANTS AND FOR ALTERING THE RESISTANCE OF PLANTS SITELE REFERENCE: 03715.0032
CURRENT FILING DATE: 1998-07-30
FRIOR APPLICATION NUMBER: 60/054,351
FRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PARCHLIN Ver. 2.1
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Sequence 1285, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-04-01
PRIOR PLING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 ELKR-DHAEMQAGCGLQTEDHLMPRRSAFASLDAV--NARLMSALTPAXRY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 17.4%; Score 57.5; DB 4; Length 260; Best Local Similarity 37.3%; Pred. No. 4.5; Matches 19; Conservative 7; Mismatches 14; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/09126420A Patent No. 6376753
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: M.catarrhalis
US-09-540-236-2236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-538-092-1285
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US-09-126-420A-20
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GENERAL INFORMATION:
APPLICANT: Griffais, R.
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
TITLE OF INVENTION: and treatment of infection
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
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Sequence 7, Application US/09499302A

GENERAL INFORMATION:
APPLICANT: BOUNG-UN, OH
APPLICANT: WOUN, KYUNG KO
APPLICANT: YOUNG, SOON KIM
TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
FILLE REFERENCE: 10324/F64430SO
CURRENT APPLICATION NUMBER: US/09/499,302A
CURRENT ELING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| :| || || || 13 || 15 || 15 || 17 || 17 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (0) ... (0) CIHER INFORMATION: Polypeptide Accession Number Q08379 US-09-538-092-1285
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1285
LENGTH: 620
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Patent No. 6559294
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DOCATION: (22)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD RES
OTHER INFORMATION: variable or unknown amino acid
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD RES
LOCATION: (49)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD RES
LOCATION: (199)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD RES
LOCATION: (226)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: WOD RES
LOCATION: (240)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: WOD RES
LOCATION: (240)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: WOD RES
LOCATION: (262)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: WOD RES
LOCATION: (262)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: WOD RES
LOCATION: (278)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: WOD RES
LOCATION: (278)
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Search completed: November 10, 2004, 12:32:32 Job tine : 20.9552 secs

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Gaps

Query Match
17.0%; Score 56; DB 3; Length 502;
Best Local Similarity 34.4%; Pred. No. 18;
Matches 11; Conservative 7; Mismatches 14; Indels

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71, Appl 325553,

sequence 32553; Sequence 53, Appl Sequence 68320, A Sequence 160144, Sequence 165777, Sequence 105777, Sequence 240457, Sequence 240457, Sequence 240457, Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 16, Appl Sequence 16, Appl Sequence 18, Appl Sequence 24, Appl Sequence 27, Appl

Sequence:

Run on:

Searched:

Database

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1 KGIISRLMSVEEELKRDHAEMQAGCGLQTEDHLMPRRSAFASLDAVNARLMSALTPAXRY
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; Sequence 20, Application US/2003003157A1
; Sequence 20, Septication No. US2003003157A1
; GENERAL INFORMATION: Philip W.
; APPLICANT: Hammond, Philip W.
; APPLICANT: Might, Martin C.
; TITLE OF INVENTION: Polypetides Interactive with BCL-X1
; TITLE PERENCE: 50036/050002
; CURRENT FILING DATE: 2002-03-07
; PRIOR PILING DATE: 2002-03-08
; WUMBER OF SEQ ID NOS: 253
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 20
: LENGTH: 67
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                                                                                                       US-10-189-346-53
US-10-282-122A-68320
US-10-282-122A-68320
US-10-437-963-106444
US-10-437-963-106477
US-10-437-963-188407
US-10-425-114-57602
US-10-425-114-57602
US-10-425-114-57602
US-10-437-963-168806
US-10-372-348-9
US-10-371-905A-12
US-10-371-905A-12
US-10-371-905A-18
US-10-371-905A-24
US-10-371-905A-24
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US-10-282-122A-69704
US-10-424-599-160165
US-10-369-493-19762
                         US-10-038-854-71
US-10-425-115-325553
US-10-189-346-52
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US-10-424-599-252794
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COCATION: 58, 62, 65
CTHER INFORMATION: Xaa = Any Amino Acid
US-10-092-750-20
   LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
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RESULT 1
US-10-092-750-20
                                                                                 \begin{matrix} \mathbf{u}_{N}\mathbf{u}_{N} & \mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N} \\ \mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}_{N}\mathbf{u}
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   g
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Sequence 108, App
Sequence 2, Appli
Sequence 24089,
Sequence 17237,
Sequence 6, Appli
Sequence 6, Appli
Sequence 1369,
Sequence 1369,
Sequence 53, Appl
Sequence 676, Appl
Sequence 676, Appl
                                                                                                                                                                                                                               (without alignments)
366.225 Million cell updates/sec
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                                                                                                                                                                                                   November 10, 2004, 15:53:52 ; Search time 64.6219 Seconds
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1 KGIISRLMSVEBELKRDHAE.....ARLMSALTPAXRYVXHCXPL
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1: /cgn2_6/ptodata/1/pubpaa/PcT_REW_PUB_PSPP:*

2: /cgn2_6/ptodata/1/pubpaa/PcT_REW_PUB_PSPP:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB_PSPP:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB_PSP:*

5: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB_PSP:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB_PSP:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB_PSP:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB_PSP:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_PSP:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_PSP:*

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13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_PSP:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_PSP:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_PSP:*

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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_PSP:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_PSP:*

19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_PSP:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_PSP:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-001-885-108
US-10-001-885-108
US-10-425-115-240989
US-10-437-963-191237
US-10-437-963-191237
US-10-311-905A-6
US-10-371-905A-6
US-10-371-905A-6
US-10-371-905A-6
US-10-371-905A-6
US-10-369-493-17471
6 US-10-369-493-17471
6 US-10-369-493-17471
6 US-10-90-925-298-676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1566620 seqs, 353225886 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Gaps ; 0

Length 67;

9

9

Result No.

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APPLICANT: Kovalic, David K. APPLICANT: Should, Thomas J. APPLICANT: Sovalic, David K. APPLICANT: Shou, Yihua APPLICANT: Shou, Yihua APPLICANT: Cao, Yongwei APPLICANT: Wei APPLICANT: Wei APPLICANT: Buckharov, Andrey A. APPLICANT: Buckharov, Andrey A. APPLICANT: Li, Ping TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE REPRENCE: 38-21(5321) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 172345
                                                                                                                                                                                                                                                                                                                                                    US-10-42-115-240989

Sequence 240989, Application US/10425115

Sequence 240989, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APOLICANT: Apolication Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 240989

LENGTH: 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 IMSVEBEL-----KRDHAEMQAGCGLQTEDHIMPRRSAFASLDAVNARIM----S 52
                                                                                 Gaps
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..
                                                                                                                                                                                              10 VEEELKRDHAEMQAGCG---LQTEDHLMPRRSAFASLDAVNARLMSALT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.6%; Pred. No. 15;
Matches 22; Conservative 11; Mismatches 24; Indels 15
    Length 964;
                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: MRT4577_151360C.1.pep
US-10-425-115-240989
    DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(183)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
Query Match 20.2%; Score 66.5; DB Best Local Similarity 36.7%; Pred. No. 14; Matches 18; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 172345, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ADVPDSTÝVSHC 112
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                            APPLICANT: Salceda, Susana
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Ju, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Profit Engrement APPLICATION NUMBER: US/10/001,885
FILE REFERENCE: DEX-0279
FILE OF INVENTION DATE: 2001-11-20
FRICH REPLIAND DATE: 2000-11-20
FRICH PRICATION NUMBER: 60/252,061
FRICH PRICATION NUMBER: 60/252,061
FRICH PRICATION NUMBER: 60/253,257
FRICH PRICATION NUMBER: 60/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Gaps
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46.8%; Score 154.5; DB 15; Length 1054;
Best Local Similarity 52.7%; Pred. No. 3.3e-11;
Matches 39; Conservative 4; Mismatches 12; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Matsumcto, Yoshiko
APPLICANT: Tsujimoto, Yoshiko
APPLICANT: Sujimoto, Gozoh
APPLICANT: Sujimoto, Gozoh
APPLICANT: Sujimoto, Gozoh
APPLICANT: Sujimoto, Gozoh
APPLICANT: Sujia, Yuji
APPLICANT: Oshida, Tadahiro
APPLICANT: Imai, Yukiho
ITILE OF INVENTION WENEN
FILE REFERENT APPLICATION NUMBER: US/10/239,734
CURRENT APPLICATION NUMBER: PCT/JP01/11286
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
NUMBER: OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GENOX RESEARCH, INC.
APPLICANT: JAPAN AS REPRESENTED BY GENEI
APPLICANT: CHILD HEALTH AND DEVELOPMENT
                                                                                                                                                                                              Sequence 108, Application US/10001885 Publication No. US20040058319A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10239734 Publication No. US20040161746A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||| |||||||||
1036 SLDAANARLMSALT 1049
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; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapien
US-10-001-885-108
                61 VXHCXPL 67
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US-10-369-493-17471

US-10-369-493-17671

US-10-369-493-17671

UURBENT APPLICANT: BAPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52022) B

CURRENT APPLICATION NUMBER: US-10/369,493

CURRENT APPLICATION NUMBER: US-60/360,039

PRIOR FILING DATE: 2003-02-28

WUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14411

LENGTH: 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hahn, Chang
APPLICANT: Liu, Hong
APPLICANT: Liu, Hong
TITLE CANT: Liu, Hong
TITLE OF INVENTION: Human Analogs of Murine Deubiquitinating Protease Genes
FILE REFERENCE: USAV2001/0185
CURRENT RILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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18.8%; Score 62; DB 14; Length 1016;
Best Local Similarity 26.2%; Pred. No. 58;
Matches 22; Conservative 12; Mismatches 26; Indels 24
                                             18.8%; Score 62; DB 14; Length 530; 26.2%; Pred. No. 26; ive 12; Mismatches 26; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                        444 NKTKPEFNVRRVEGTVPPDVLVIH 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930 NKTKPEFNVRRVEGTVPPDVLVIH 953
                                                                                                                                                                                                                                                                                                                                                                  45 ----AVNARLMSALTPAXRYVXH 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 4, Application US/10371905A; Publication No. US20030224969A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: human DUB4.1a
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ORGANISM: Bacillus halodurans
US-10-369-493-17471
                                                                                          Best Local Similarity 26.2
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1016
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-371-905A-4
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                                                     Query Match
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
ITTLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
ITTLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 191237
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Sequence 6, Application US/10371905A
Publication No. UG20030224969A1
GENERAL INFORMATION:
APPLICANT: Hahn, Chang
APPLICANT: Liu, Hong
ITILE OF INVENTION: Human Analogs of Murine Deubiquitinating Protease Genes
FILE REFERENCE: USAV2001/0185
FILE REFERENCE: USAV2001/0185
CURRENT APPLICATION NUMBER: US/10/371,905A
CURRENT APPLICATION NUMBER: US/10/371,905A
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 530
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                            6 RLMSVEEELKRDHAEMQAGCGL-----QTEDHLMPRRSAFA 41
                                                                                                                                                                                                                                                                                                                                                                      41 RAAELEERLRQVAAESQAWCGLARSNEAVAAGIRATLDHLLLRAAAAA 88
                                                                                                                                        Length 183;
                                                                                                                                                                                                              13; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70490C.1.pep
US-10-437-963-172345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION; Clone ID: PAT_MRT4530_87574C.1.pep
US-10-437-963-191237
                                                                                                                               Score 63; DB 16;
Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(203)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 191237, Application US/10437963
, Publication No. US20040123343A1
, GENERAL INFORMATION:
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; OTHER INFORMATION: human DUB4.1b
US-10-371-905A-6
                                                                                                                               Query Match
Best Local Similarity 37.5%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
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Best Local Similarity 31.3%; Pred. No. 22;
Matches 21; Conservative 8; Mismatches
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Sequence 676, Application US/09925298
Publication No. US20020039764A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                             6 RLMSVEEELKRDH-----AEMQAGCGLQTEDHLMPRRSA--FASLDAVNARLMSALTP 56
                                                  Gaps
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Publication No. US20040101874A1

General INFORMATION:

APPLICANT: Ghosh, Sounitra S.

APPLICANT: Tably, Bing

APPLICANT: Tablo, Bring

APPLICANT: Tablo, Brader W.

APPLICANT: Tablo, Brader E.

APPLICANT: Marnock, Dale E.

BROWNER OF SEQ ID NOS: 3077

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 1369

LENGTH 401
                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18.6%; Score 61.5; DB 16; Length 401; Best Local Similarity 31.3%; Pred. No. 22; Matches 21; Conservative 8; Mismatches 29; Indels 9
     Length 395;
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                                                  Indels
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US-09-782-816A-53
Sequence 53, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION;
FILE REFERENCE: UC069,001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT PILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
LENDAL: 406
  Query Match 18.6%; Score 61.5; DB 14; Best Local Similarity 26.2%; Pred. No. 21; Matches 22; Conservative 10; Mismatches 27;
                                                                                                 2 GIISRLMSVEEEL -- KRDHAEMQAGCGLQTEDHLMPRRS
                                                                                                                                                                                                                                      176 VDALFSMDGDHANLHDLVTLKERY 199
                                                                                                                                                                                           39 -- AFASLDAVNARLMSALTPAXRY 60
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ORGANISM: Homo sapiens
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LOCATION: (5)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE

LOCATION: (6)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE

LOCATION: (16)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-298-676
                                                                                       6 RIMSVEBELKRDH-----AEMQAGCGLQTEDHLMPRRSA--FASLDAVNARLMSALTP 56
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9; Gaps
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Sequence 676, Application US/10102806

Sequence 676, Application US/10102806

GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFRENCE: PA103PIC1

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO3
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR PLICATION NUMBER: PCT/US00/05881
PRIOR PLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
NUMBER OF SEQ ID NOS: 8466
SOFTWARE: PATENTION OF SEC ID NOS: 8466
29; Indels
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Spytek, Kimberly A

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LOCATION: (6)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                             FEATURE:
OAMBIKEY: SITE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-102-806-676
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 31.3%; Pred. No. 26;
Matches 21; Conservative 8; Mismatches 29; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1222.

Sequence 1222.

Publication No. US2020182586A1

Publication No. US2020182586A1

APPLICANT: MORATION.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVER 2002-03-01

PRIOR FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 2059

SOFTWARE FLAKE PRIOR SEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 2028

LENGTH: 2446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 71, Application US/10038854; Publication No. US20040022781A1; GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 676
LENGTH: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-087-192-2028
                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 VNEIAKH 360
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US-10-038-854-71
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APPLICANT: Wolence, Ada. R
APPLICANT: Wolence, Ada. R
APPLICANT: Wolence, Ada. R
APPLICANT: Wolence, Ada. R
APPLICANT: Anyanka. Currel M
APPLICANT: Anyanka. Currel M
APPLICANT: Shinkee, Richard A
APPLICANT: Shinkee, Richard B
APPLICANT: Shinkee, Shinkee B
APPLICANT: Shinkee B
AP
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O'GEN HIDE GOESHILL

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 11:36:51; Search time 13.5448 Seconds (without alignments) 475.942 Million cell updates/sec Run on:

US-10-092-750-20 Title: Perfect sc Sequence:

330 1 KGIISRLMSVEBELKRDHAE.....ARLMSALTPAXRYVXHCXPL score:

Scoring table:

BLOSUM62 Gapop 10.0., Gapext

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Ras-GTPase activat	ras GTPase-activat	CDA peptide synthe	8-amino-7-oxononan	HIV-EP2 enhancer-b	tical	14	hypothetical prote	₽	clpB heat shock pr	_	hypothetical prote	Έ.	hypothetical prote	_	probable sorbitol	ated	head-to-tail joini	sporulation initia	hypothetical prote	cytochrome P450 71	cytochrome P-450LX	95K golgi antigen	hypothetical prote	hypothetical prote		О	c	centrosome associa
		T14270	T14259	T36180	C84138	WMHUE2	F84182	F81692	T23310	H82751	T51523	T16511	T46211	AH0042	T16270	T22934	T34660	B41870	JQBPT7	D83801	QQBET1	A35867	T52256	JH0821	820531	G86496	B81546	24	806997	980
	DB	10	N	~	~	н	~	7	N	~	~	~	~	~	~	~	~	(1	Н	~1	Н	H	N	7	~	7	~	~	0	N
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æ	Query Match	21.8	ä	φ.	œ,		œ.	18.2	œ,	7	7	۲.	۲.	17.7	17.7	•	17.6	17.4	17.4	•	•		17.3	17.3	17.3	~	17.1		17.1	17.1
	Score	72	72	63		61.5	60.5	9	59.5	59	53	59	æ	58.5	æ	58	28	57.5	7	57	57	57	57	57	57	56.5	9	9	56.5	ġ
		н	7	m	4	S	9	7	80	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Gaps

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1245 KSIIGRLMLVEBELRRDHPAM 1265

1 KGIISRLMSVEEELKRDHAEM 21

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thiamin biosynthes	ribose-phosphate p	hypothetical prote	breast cancer tumo	breast cancer susc	breast cancer tumo	probable D-isomer	hypothetical prote	hypothetical prote	probable membrane	probable adenine d	protein kinase (EC	myosin V - fruit f	type III export pr	glucuronosyltransf	probable propionyl	
AH0932	T41036	T21556	T30835	T42205	T30904	AC0337	D90880	E85738	E64892	H95379	A46590	T13939	E83431	A39092	F75382	ALIGNMENTS
(1)	N	N	N	~	N	N	N	N	N	N	н	N	N	N	N	
252	321	369	3328	3329	3329	375	585	585	585	600	762	1792	214	533	558	
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17	17.	17	17	17.0	17	16	16	16.8	16	16	16	16	16	16.7	16	
9 '	26	56	56	56	56	55.5	55.5	55.5	55.5	55.5	55.5	55.5		ວ		

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Nilternate names: profein SynGAP
Cispecies: Rattus norregicus (Norway rat)
Cispecies: 10.68p-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cispecies: Table Data Library, February 1998
Submitted to the EMBL Data Library, February 1998
Submitted to the EMBL Data Library, February 1998
A; Personce number: 217942
A; Reference number: 21794
Ras-Grpase activating protein SynGAP-b - rat
C,Species: Rattus norvegicus (Norway rat)
C,Species: Rattus norvegicus (Norway rat)
C,Species: Rattus norvegicus (Norway rat)
C,Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C,Accession: T14270
R;Kim, J.H.; Liao, D.; Lau, L.F.; Huganir, R.L.
R)Weuron 20, 683-661, 1998
A,Title: SynGAP: a synaptic RasGAP that associates with the PSD-95/SAP90 protein family.
A,Reference number: Z17950; MUID:98240917; PMID:9581761
A,Accession: T14270
A,Accession: T14270
A,Accession: preliminary; translated from GB/EMBL/DDBJ
A,Accession: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-1249 <KIM>A,Coss-references: EMBL:AF058790; NID:g3722228; PIDN:AAC63511.1
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T14259
ras GTPase-activating protein, synaptic - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1201 KSIIGRLMLVEBELRRDHPAM 1221
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CDA peptide synthetase III

Status: preliminary; translated from GB/EMBL/DDBJ

A; Gene: cdaPS3; SCOEDB: SCE63.01

Query Match
Best Local Similarity 39.6%;
Matches 19; Conservative

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Dypothetical protein Vng0219h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Perb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: F84182
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, W.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniells, C.J.; Dennells, C.J.; Denn
                                                                                                                                                                                                                                                                                            A,Map position: 6923-6924
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA binding; duplication; metal binding; transcription regulation; zinc finge
F;245-295/Region: DNA binding #status predicted
F;245-265/Region: zinc finger CCHH motif
F;273-295/Region: zinc finger CCHH motif
F;991-997/Region: nuclear location signal
C,Date: 31-Mar-1993 #sequence revision 07-Jul-1995 #text_change 09-Jul-2004
C,Accession: $26661, A39829; $38253
C,Accession: $26661, A39829; $38253
Exyan't Veer, L.J.; Lutz, P.M.; Isselbacher, K.J.; Bernards, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 8971-8975; 1992
A,Title: Structure and expression of major histocompatibility complex-binding protein 2, A,Reference number: $26661; MUID:93028387; PMID:1409593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 668-2144, K; 2146-25500 <NOM>
A; Residues: 668-2144, K; 2146-25500 <NOM>
A; Cross-references: GB:M60119; NID:95661140; PIDN:AAB88218.1; PID:9182120
R; Rustgi, A.K.; Van't Veer, L.J.; Bernards, R.
Proc. Natl. Acad. Sci. U.S.A. 87, 8707-8710, 1590
A; Title: Two genes encode factors with NF-kappaB- and H2TF1-like DNA-binding properties.
A; Reference number: A38253; MUID:91062349; PMID:2247438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: mRNA
A,Residues: 1851-1990 <RUS>
A,Cross-references: GB:M61744; GB:M33920; NID:g187404; PIDN:AAA36202.1; PID:g187405
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F;1852-1908/Region: DNA binding #status predicted
F;1852-1875/Region: zinc finger CCHH motif
F;1883-1997/Region: zinc finger CCHH motif
F;1953-1977/Region: acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
18.6%; Score 61.5; DB
Best Local Similarity 25.8%; Pred. No. 65;
Matches 17; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: GDB:HIVEP2
A,Cross-references: GDB:129086; OMIM:143054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown
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1583 VSPSSR 1588
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A,Status: preliminary
A,Molecule type: DNA
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R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M. SyReference number: 221600

A;Reference number: Z21600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Wolecule type: DNA
A;Residues: 1-211 <211 <314
A;Cross-references: UNIPROT:08CJX2; EMBL:AL035707; PIDN:CAB38876.1; GSFDB:GN00070; SCOED
A;Experimental source: strain A3(2)
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirs
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C84138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9K625; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB076
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV-EP2 enhancer-binding protein - human
N;Alternate names: finger protein, 275K; human immunodeficiency virus enhancer-binding
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8-amino-7-oxononanoate synthase bioF [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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                                                                                                                                                             Species: Streptomyces coelicolor
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: carrier protein; phosphopantetheine; phosphoprotein F;208-662/Domain: acetate-CoA ligase homology <ACLI>F;678-746/Domain: acyl carrier protein homology <ACLI>F;128-1725/Domain: acyl carrier protein homology <ACLI>F;1280-1725/Domain: acetate-CoA ligase homology <ACL2>F;1740-1808/Domain: acyl carrier protein homology <ACPS>F;1740-1808/Domain: acyl carrier protein homology cachier F;710,1772/Binding site: phosphopantetheine (Ser) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 DHAEMQAGCGLQTEDHLMPRRSAFASLDAV----NARLMSALTPAXRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 395;
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Pred. No. 35;
5; Mismatches 18; Indels
                                                                                                                     Streptomyces coelicolor (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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2 GIISRLMSVEEEL --- KRDHAEMQAGCGLQTEDHLMPRRS-

D $\dot{\delta}$ g

VDÁLFSMDGDHÁNLHDLVTLKERY 199 --AFASLDAVNARLMSALTPAXRY 60

RESULT 5

27; 5;

18.6%; Score 61.5; DE 26.2%; Pred. No. 8.1; Live 10; Mismatches

Conservative

Query Match Best Local Similarity Matches 22; Conserv

A;Molecule type: DNA A;Residues: 1-395 <STO> Status: preliminary

A;Gene: bioF

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A,Status: new.oi.
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-708 6.21M>
A,Residues: 1-708 6.21M>
A,Residues: 1-708 6.21M>
A,Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
B;Experimental 9a5c
B;Experime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-dependent helicase XF0882 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Bate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82751
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc Nature 406, 151-157, 200
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A8515; MuID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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1 KGIISRLMSVEEELKRDHAEMQAGGGLQTEDHLMPRRSAFASLDAVNARLMSALTPAXRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.9%; Score 59; DB 2; Length 708; Best Local Similarity 34.4%; Pred. No. 32; Matches 21; Conservative 10; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                             776
                                                                                                                                                                                         45 AVN 47
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774 SIN '
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Typerate of the control of 
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A,Status: preliminary
A,Notesidus: preliminary
A,Residus: 1-456 <TET>
A,Cross-references: UNIPROT:Q9FKE4; GB:AE002321; GB:AE002160; NID:g7190560; PIDN:AAF3936
A,Experimental source: strain Nigg (MoPn)
C,Genetics:
A,Gene: TC0521
C;Superfamily: replication initiation protein dnaA
                         A;Cross-references: UNIPROT:Q9HSIO; GB:AE004437; NID:g10579866; PIDN:AAG18826.1; GSPDB:G
C;Genetics:
A;Gene: VNG0219H
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A;Gene: CESP:K04D7.5
A;Map position: 4
A;Introns: 28/2; 116/3; 153/3; 270/1; 351/3; 579/3; 699/3; 1002/3; 1024/3; 1080/3; 1132/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosomal replication initiator protein DnaA TC0521 [imported] - Chlamydia muridarum (C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: F81692 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
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Best Local Similarity 27.0%; Pred. No. 57;
Matches 17; Conservative 9; Mismatches 18; Indels 19
                                                                                                                                                                                                                                                                                                                   Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                         30; Indels
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18.2%; Score 60; DB 2; Length 456
Best Local Similarity 33.3%; Pred. No. 15;
Matches 15; Conservative 9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                ch
1 Similarity 32.8%; Pred. No. 4.6;
20; Conservative 10; Mismatches
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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A;Residues: 1-185
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Cidate: 02-Nov-2001 #Sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
Cidatession: AH0042
CiAccession: AH0042
Ribarkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F.
Nature 413, 523-527, 2001
A; Ritherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, F.
Nature 413, 523-527, 2001
A; Reference number: AB0001; WUD:21470413; PMID:11586360
A; Reference number: AB0001; WUD:21470413; PMID:11586360
A; Residues: Dreliminary
A; Molecule type: DNA
A; Residues: 1-715 < KUR>
A; Residues: 1-715 < KUR>
C; Genetics:
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A;Residues: 1-1827 <FUL>
A;Cross-references: UNIPROT:Q20042; EMBL:U29381; NID:g868214; PID:g868224; PIDN:AAA68757.
A;Experimental source: strain Bristol N2
C;Genetics: A;Gene: CESP:F35D11.11
A;Gene: CESP:F35D11.11
A;Introns: 76/2; 131/3; 159/3; 185/3; 221/3; 253/3; 320/1; 869/3; 1133/3; 1205/2; 1250/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Species: Yersinia pestis
C,Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T22934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
17.7%; Score 58.5; DB 2; Length 1827;
Best Local Similarity 25.4%; Pred. No. 1.18+02;
Matches 18; Conservative 15; Mismatches 25; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 LOTEDHIMPRRSAFASLDAV------NARLMSALTPAXRYVXH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58.5; DB 2;
Pred. No. 37;
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A,Molecule type: DNA
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submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: fdhF
C;Superfamily: formate dehydrogenase
C;Keywords: oxidoreductase
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Best Local Similarity 34.8%;
Matches 16, Conservative 5
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1672 EREISALKRHV 1682
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R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; submitted to the Protein Sequence Database, December 1999
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C,Species: Caenorhabditis elegans
C,Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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17.7%; Score 58.5; DB 2; Length 644;
Best Local Similarity 26.3%; Pred. No. 33;
Matches 15; Conservative 14; Mismatches 21; Indels
A;Introns: 76/3; 149/3; 229/1; 294/2; 312/3; 363/1; 466/1; 862/3
A;Note: T20K14_60
C;Superfamily: endopeptidase Clp ATP-binding chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.9%; Score 59; DB 2; Length 1387; 32.8%; Pred. No. 68;
                                                                                                              Length 968;
                                                                                                        17.9%; Score 59; DB 2; Length 968
28.1%; Pred. No. 45;
tive 15; Mismatches 23; Indels
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-644 - CCHO>
A;Cross-references: UNPROT:09SMN2; EMBL:AL133315
A;Experimental source: cultivar Columbia; BAC clone T8P19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, December 1995
A; Description: The sequence of C. elegans cosmid F59A6.
A;Reference number: Z18526
A;Accession: T16511
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A;Residues: 1-1387 <NHA>
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A;Introns: 133/1; 373/3; 403/3; 496/3; 566/3
A;Introns: 123/1; 373/3;
                                                                                                              Query Match
Best Local Similarity 28.1%
Matches 18; Conservative
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A,Reference number: 219639
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A,Accession: T22934
A,Accession: T22934
A,Molecule type: DNA
A,Residues: 1-354 <MIL>
A,Ferperimental source: clone F58G1
C,Genetics: CESP:F8G1.2
A,Rene Dosition: 2
A,Rep position: 2
A,Introns: 135/3; 301/3
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Best Local Similarity 27.7%; Pred. No. 19;
Matches 13; Conservative 10; Mismatches 18; Indels
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Search completed: November 10, 2004, 12:29:25 Job time : 14.5448 secs

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1 KGIISRLMSVEEELKRDHAE......ARLMSALTPAXRYVXHCXPL
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SEQUENCE FROM N.A.
STRANT-E57BL/6
STRANT-E57BL/6
MEDLINE=22760439; PubMed=12877983;
Homayouni R., Magdaleno S., Keshvara L., Rice D.S., Curran T.;
"Interaction of Disabled-1 and the GTPase activating protein Dab2IP in mouse brain.";
Brain Res. Mol. Brain Res. 115:121-129(2003).

AAP31233 PRELIMINARY; PRT; 475 AA.
02-MAR-2204 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
MAS-interacting protein (Fragment)
Mus musculus (Mouse)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
11)

P31629 homo sapien C9nsC5 homo sapien C02646 homo sapien C9r0m0 mus musculu C9gduB heliobacteri C991n1 mus musculu C8c91 mus musculu C8c71 mus musculu C7tsr5 mus musculu C6c2pg9 mus musculu		date) update)	ebrata; Euteleostomi; Muridae; Murinae; Mus.	activating protein Dab2IP in	447 CRC64;	DB 2; Length 475; .0; .14; Indels 1; Gaps 1;	KGIISRLMSVEEELKRDHAEMQAGCGLQTEDHLMPRRSAFASLDAVNARLMSALT 55 	
1 ZEP2 HUMAN 2 Q9NSOS 2 Q02646 2 Q02646 2 Q9GDUS 2 Q9HN1 2 Q8C916 2 Q8C916 2 Q8C916 2 Q8C916 2 Q8C916 2 Q8C916 2 Q8C90 2 Q8C90 2 Q8C90 2 Q8C90 2 Q8C90 3 Q8C90 3 Q8C90 4 Q8C90 5 Q8C9	ALIGNMENTS	PRT; 475 AA. 27, Created) 27, Last sequence update) 27, Last annotation updat	ata; Craniata; Vertebrata; E tia; Sciurognathi; Muridae;	777983; Keshvara L., F ind the GTPase	. 115:121-129(2003). 1; - binding; IPI. MW; 5199721C6D7CF447	s; Score 153.5; b; Pred. No. 3e-1 4; Mismatches	DHAEMQAGCGLQTEDHLMP DHAEMQAAVD-SKQKIIDA	
18.6 2446 118.6 2446 118.6 2450 118.5 2950 118.3 185 118.3 929 118.3 954 118.3 964 118.3 970		ARY; el. el.	(hetazoa; Chordata; Itheria; Rodentia;	FFCOM N.A. 57BL/6; 22760439; PubMed=128 18., Magdaleno S., tion of Disabled-1 a	Mol. Brain Res. 784, AAP31233.1 515, F:protein 1 1 1 475 AA; 51159	46.59 Similarity 65.59 6; Conservative	[ISRLMSVEEELKR 	
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"Differential regulation of the human gene DAB2IP in normal and malignant prostatic epithelia: cloning and characterization."; Genomics 79:573-581(2002).

EMBL, AF367051; AAM00371.1; -.

HSSP; P21359; INF1.

InterPro; IPR0000008; C2.

InterPro; IPR000936; RasGAP.

InterPro; IPR001936; RasGAP.

InterPro; IPR001936; RacGAP.

Pfam; PF00168; C2; I.

Pfam; PF00168; C2; I.
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EMBL; AY305658; AAQ77381.1; -.
EMBL; AY305656; AAQ77379.1; -.
GO; GO:0005515; F.protein binding; IPI.
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InterPro; IPR001936; RasGAP.
InterPro; IPR008936; Rho_GAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL_2004 (TrEMBLrel. 27, 05-JUL_2004 (TrEMBLrel. 27, 01-OCT-2004 (TrEMBLrel. 28, DAB2IP.
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Pfam; PF00616; RasGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000008; C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q6P730;
05-JUL-2004 (
05-JUL-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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Q6JTV1
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Q6P730
               RAH DAKA BARKA BAR
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Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
Nakazima D., Nagase T., Ohara O., Kaga H.,
"Prediction of the coding sequences of mouse homologues of KIAA gene:
II. The complete nucleotide sequences of mouse KIAA-homologus
cDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries.";
DNA Res. 10:35-48(2003).
EMBL; AK122548; BAC55830.1; -
MGD; MGI:2548; BAC55830.1; -
MGD; MGI:2548; BAC55830.1; -
INTERPO: IPRO01936; RasGAP.
InterPro: IPRO01936; RasGAP.
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                       1 KGIISRLMSVEEELKRDHAEMQAGCGLQTEDHLMPRRSAFASLDAVNARLMSALT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KGIISRLMSVEEELKRDHAEMQAGCGLQTEDHLMPRRSAFASLDAVNARLMSALT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                       ;;
                                                                                                                          Query Match 46.5%; Score 153.5; DB 2; Length 475; Best Local Similarity 65.5%; Pred. No. 3e-10; Matches 36; Conservative 4; Mismatches 14; Indels 1
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65.5%; Pred. No. 5.4e-10;
tive 4; Mismatches 14; Indels 1.
      EMBL; AY178784; AAP31233.1; -.
NON TER 1 1
SEQUENCE 475 AA; 51159 MW; 5199721C6D7CF447 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Last annotation update)
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SMART; SM00323; RasGAP; 1.
PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
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MEDLINE=21945266; PubMed=11944990;
Chen H., Pong R.C., Wang Z., Haieh J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBTDL2;
01-JUN-2002 (TrEWBLrel. 21, Created)
01-JUN-2002 (TrEWBLrel. 21, Last seq
01-OCT-2003 (TrEWBLrel. 25, Last and
DOC-2/DAB2 interactive protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Dab2ip; Synonyms=mKIAA1743;
Mus musculus (Mouse).
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Best Local Similarity 65.59
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                             Query Match
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Q80T97;
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Q80T97
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Gaps
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                                                                                                                                                                                                                                                           1 KGIISRLMSVEBELKRDHAEMQAGCGLQTEDHLMPRRSAFASLDAVNARLMSALT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-Dablip;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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STRAILH-12986/SvPvTac; TISSUB=Spleen;
Chen H., Karam J.A., Hsieh J.-T.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
SMART; SM00239; C2; 1.
SMART; SM0323; RasGAP; 1.
PROSITE: PSSO018; RAS GTPASE ACTIV 2; 1
SEQUENCE 967 AA; 106751 NW; 22536D86167137D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00239; C2; 1.
SMART; SM00323; RasGAP, 1.
PROSITE; PS50018; RAS GTASE ACTIV 2; 1.
SEQUENCE 996 AA; 109994 WW; FD31F282048F9BF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                     / Match 46.5%; Score 153.5; DB 2; Local Similarity 65.5%; Pred. No. 6.6e-10; les 36; Conservative 4; Mismatches 14;
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46.5%; Score 153.5; DB 2;
Best Local Similarity 65.5%; Pred. No. 6.8e-10;
Matches 36; Conservative 4; Mismatches 14;
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SEQUENCE FROM N.A.
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Best Local
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Atlausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Bottchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Woslen T.B., Tooshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wosley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Rahay J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Brodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

C. Marza M.J., Salska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marza M.A.,

T. "Generation and initial analysis of more than 15,000 full-length human
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;
                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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SEQUENCE FROM N.A.
MEDLINE=21935348; PubMed=11812785;
Wang Z., Tseng C.P., Pong R.C., Chen H., McConnell J.D., Navone N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KGIISRIMSVEEELKRDHAEMQAGGGLQTEDHLMPRRSAFASLDAVNARLMSALT
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Pred. No. 6.8e-10;
4; Mismatches 14; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases. BMBL; BC061865; A4H61865.1; -. InterPro; IPR000008; C2. InterPro; IPR0008973; C2 CalB. InterPro; IPR001936; RasGAP. InterPro; IPR001836; RasGAP.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Dab2ip protein.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SMART; SM00323; RasGAP; 1.
SMO03213; PS50018; RAS GTPASE ACTIV 2; 1.
SEQUENCE 996 AA; 110004 MW; CAĞB43DE
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Pfam; PF00616; RasGAP; 1.
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Matches 36; Conservative
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                                                                                                                                                              NCBI_TaxID=10116;
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10924M9
10026
AC 0924M
DT 01-D
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DT 01-D
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MEDINE=223825; PubMed=12477932;

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Hsieh J.T.;
"The mechanism of growth-inhibitory effect of DOC-2/DAB2 in prostate cancer. Characterization of a novel GTPase-activating protein associated with N-terminal domain of DOC-2/DAB2.";
J. Biol. Chem. 277:12622-12631(2002).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00239; C2; 1.
SMART; SM00323; RasGAP; 1.
PROSITE; PSS0018; AAS GTPASE ACTIV 2; 1.
SEQUENCE 996 AA; 110075 NW; B4DF6755548ED9EC CRC64;
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Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                          HMBL; AF236130; AAK93947.1; -... HSSP; P21359; 1NF1.
INCEPTO; IPROCOO09; C2.
INCEPTO; IPROCOO93; C2. Calb.
INTERPO; IPRO01936; RasGAP.
InterPro; IPRO01936; RasGAP.
Pfam; PF00169; C2; 1.
Pfam; PF00169; RasGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 46.5%;
1 Similarity 65.5%;
36; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences.
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                                                                                                                                                                                                                     Zhi W.;
Submitted (FEB-2000)
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STRAIN=12956/SvEvTac; TISSUE=Spleen;
Chen H., Karam J.A., Hsieh J.-T.;
"Cloning and characterization of mouse DAB2IP gene and its promoter.";
submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY305658; AAG77381.1; -.
SEQUENCE 996 AA; 109994 MW; FD31F282048F9BF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
MEDIINE=21082932; PubMed=11214970;
MEDIINE=21082932; PubMed=11214970;
Magaze T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
Magaze T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
EMBL; AB051530; BAB21834.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        907 KGIISRLMSVEEELKKDHAEMQAAVD-SKQKIIDAQEKRIASLDAANARLMSALT 960
                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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01-077-2002 (TrEMBLrel. 22, Last sequence update)
10-077-2003 (TrEMBLrel. 25, Last annotation update)
KIAA1743 protein (Fragment).
                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
46.5%; Score 153.5; DB 2;
Best Local Similarity 65.5%; Pred. No. 6.8e-10;
Matches 36; Conservative 4; Mismatches 14;
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                                                        996 AA
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PROSITE; PSS0018; RAS GTPASE_ACTIV_2; 1.
NON_TER 1 1.
SEQUENCE 1036 AA; 114409 MW: 1B07D8N?
                                                                                              Created)
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InterPro; IPR008973; C2_CalB.
InterPro; IPR01849; PH.
InterPro; IPR011036; PH_related.
InterPro; IPR01936; RasGAP.
InterPro; IPR008936; Rho_GAP.
                                                                                      01-00N-2004 (TrEMBLrel. 27, 01-00N-2004 (TrEMBLrel. 27, 01-00N-2004 (TrEMBLrel. 27, DAB2IP.
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SMART; SM00323; RasGAP; 1.
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Pfam; PF00169; PH; 1.
Pfam; PF00616; RasGAP; 1.
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                                                     PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                 RESULT 11
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STRAIN=12956/SWCTac; TISSUB=Spleen;
STRAIN=12956/SWCTac; TISSUB=Spleen;
Chen H., Faram J.A., Hsieh J.-T.;
"Cloning and characterization of mouse DAB2IP gene and its promoter.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY3056556; AAQ77379-11;
SEQUENCE 996 AA, 109994 WW; FD31F282048F9BF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STEATM=12956/SVEVTac; TISSUE=Spleen;
Chen H., Karam J.A., Hsieh J.-T.;
"Cloning and characterization of mouse DAB2IP gene and its promoter.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY305657; AAQ77380.1; -.
SEQUENCE 996 AA; 109994 WW; PD31F282048F9BF8 CRC64;
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                                                                                                                                       1 KGIISRLMSVEEELKRDHAEMQAGCGLQTEDHLMPRRSAFASLDAVNARLMSALT 55
                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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DABZIP.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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46.5%; Score 153.5; DB 2; Length 996;
Best Local Similarity 65.5%; Pred. No. 6.8e-10;
Matches 36; Conservative 4; Mismatches 14; Indels 1;
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Best Local Similarity 65.5%; Pred. No. 6.8e-10;
Matches 36; Conservative 4; Mismatches 14; Indels 1;
                                                          DB 2; Length 996;
                                                   Query Match 46.5%; Score 153.5; DB 2; Length Best Local Similarity 65.5%; Pred. No. 6.8e-10; Matches 36; Conservative 4; Mismatches 14; Indels
EMBL; BC061865; AAH61865.1; -. SEQUENCE 996 AA; 110004 MW; CA6B43D3129F4D6E CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
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AAQ77380;
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AAQ77379;
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RESULT 10

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AAC77380

ID AAC7

DT 01-0

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7

Gaps

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DAB2IP

RESULT 9 AAQ77379

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PH.
C2 domain.
Ras-GAP.
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EMBL; AL035702; CAB53260.1; -.
HSSP; P21359; INF1.
FEBS Lett. 441:127-131(1998).
                                                    SEQUENCE OF 41-1139 FROM N.A.
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                                                                              Chapman J.;
Submitted (AUG-1999)
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922 92
1139 AA;
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Best Local
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GAP2_DROME
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                                                                                 976 KGIISRLMSVEBELKKDFAEMQAAVD-SKQKIIDAQEKRIASLDAANARLMSALT 1029
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L6-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

Kas GTPase-activating protein nGAP (RAS protein activator like 1).

Name-RASAL2; Synonyms-NGAP;

Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                    1 KGIISRLMSVEBELKRDHAEMQAGCGLQTEDHLMPRRSAFASLDAVNARLMSALT
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MEDLINE=99093006; PubMed=9877179;
Noto S., Maeda T., Hattori S., Inazawa J., Imamura M., Asaka M.,
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Pred. No. 7.3e-10;
4; Mismatches 14; Indels 1;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Schuuring B.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AV013952; AAK50336.1;
Genew, HGNC:17294; DAB21P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                    Created)
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InterPro; IPR0009973; C2_CalB.
InterPro; IPR001849; PH. related.
InterPro; IPR00136; PH related.
InterPro; IPR001936; RasGAP.
InterPro; IPR008936; Rho_GAP.
Pfam; PP00168; C2; 1.
Pfam; PF00168; PH; 1.
                                                                                                                                                                                                                                                                    O96SE1,
01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 65.5%;
Matches 36; Conservative
36; Conservative
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                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hatakeyama M.;
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NOAP HUNAN
NO AD HUNAN
NO SOUGE
DT 16-OCT
DT 16-OCT
DT 05-UUL
DE Rass GT
GN Annes HOMO 8.
OC BURKALY
OC MARKALY
OC MARKALY
OC MARKALY
CO MARKALY
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10,668E1
10,068E1
10,01-DE
DT 01-DE
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  Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNEL cutstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license@isbement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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to the EMBL/GenBank/DDBJ databases.
tory regulator of the Ras-cyclic AMP pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.8%; Score 131.5; DB 1; Length 1139; 56.4%; Pred. No. 4.1e-07; tive 7; Mismatches 16; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dronomica de la proposater (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 Poly-Lys.
25 Poly-Ser.
128556 MW; 4A65C8243E1259A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIN, 606136; ...
MIN, 606136; ...
MIN, 606136; ...
GO; GO:000599; F:Ras GTPase activator activity; TAS.
GO; GO:000196; P:signal transduction; TAS.
INTERPRO; IPRO0009; C2.
INTERPRO; IPRO01949; PH. related.
INTERPRO; IPRO01936; PH. related.
INTERPRO; IPRO01936; RasGAP.
INTERPRO; IPRO01936; RasGAP.
Fram; PRO0616; RasGAP; I.
Fram; PRO0616; RasGAP; I.
SMART; SM00233; PH; I.
SMART; SM00323; PH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00499; C2_DOMAIN 1; FALSE_NEG.
PROSITE; PS50004; C2_DOMAIN 2; FALSE_NEG.
PROSITE; PS50003; PH_DOMAIN; FALSE_NEG.
PROSITE; PS50018; RAS_GTPASE_ACTIV_1; FALSE_NEG.
PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAP2_DROME STANDARD; PRT; 1556 AA. 081498; Q95TL0; Q9YX23; 10-OCT-2003 (Rel. 42, Crated) 110-OCT-2003 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 05-Dable sas GTPase-activating protein. ORFNames=CG32560;
                                 -i- FUNCTION: Inhibitory regulator of the R-i- SIMILARITY: Contains I C2 domain.
-i- SIMILARITY: Contains I PH domain.
-i- SIMILARITY: Contains I Ras-GAP domain.
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REP STOURNER FROM N.A.

REPUBLIANE STROWN STRONG STRO
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayrakaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS
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SEQUENCE FROM N.A.

STRAIN=Berkeley; TISSUB=Embryo, and Testis;

MEDLINE=22426066; PubMed=12537569;

A Stapleron M., Carlson U.W., Broketein P., Yu C., Champe M.,

A George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,

A Rubin G.M., Celniker S.E.;

A Drosophila full-length CDNA resource.";

Genome Biol. 3.RESEARCH0080.1-RESEARCH0080.8(2002).

I PONCTION: Probable GTPase-activating protein, which may act as a negative regulator for some member of the Ras family. They decrease the signaling activity of Ras by stimulating its intinsic GTPase activity, thereby lowering the levels of GTP-bound, active Ras (By similarity).

C -- SUBCELIULAR LOCATION: Cytoplasmic (By similarity).

-- SIMILARITY: Contains 1 Ras-GAP domain.

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                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005737; C:cytoplasm; ISS.
GO; GO:0005737; C:cytoplasm; ISS.
GO; GO:000509; F:Ras GTPase activator activity; ISS.
GO; GO:00046580; P:negative regulation of RAS protein signal t. . .; ISS.
InterPro; IPR000008; C2.
InterPro; IPR001849; FH.
InterPro; IPR011036; PH related.
InterPro; IPR011036; RASGAP.
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ches 17; Indels 3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

27.4%; Score 90.5; DB 1; Length 1556;
Best Local Similarity 39.3%; Pred. No. 0.067;
Matches 22; Conservative 14; Mismatches 17; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1403 1411 Polý-Gly.
1540 1547 Poly-Cln.
1346 145 H -> Pin Ref. 3; AAL90028).
1356 AA; 170797 MW, 1EA002B6DFF7D7F8 CRC64;
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Ras-GAP.
Roly-Lys.
Poly-Cily.
Poly-Gilv.
                                                                                                                                                                                                                                                     EMBL, AE003506, AAF48759.2; -.
EMBL, AY058706; AAL13935.1; -.
EMBL, AY089290; AAL90028.1; ALT_INIT.
ILILACt; Q87498; -.
FlyBase; FBGN0052560; CG32560.
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1192
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Search completed: November 10, 2004, 12:27:24 Job time : 75.3071 secs

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Sequence 1246 Appli
Sequence 1246 Appli
Sequence 16, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
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Sequence 6, Appli
                                                           November 10, 2004, 11:41:17; Search time 7.74383 Seconds (without alignments) 222.664 Million cell updates/sec
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                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/taa/5A_COMB.pep:*
/cgn2_6/ptodata/1/taa/5B_COMB.pep:*
/cgn2_6/ptodata/1/taa/6A_COMB.pep:*
/cgn2_6/ptodata/1/taa/6B_COMB.pep:*
/cgn2_6/ptodata/1/taa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/taa/PCTUS_COMB.pep:*
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                  1 WERIEERLAYIADHLGFSWTELARAL 26
                                                                                                                                                                 478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           protein search, using sw model
                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                    seq length: 0
seq length: 200000000
                                                                                                US-10-092-750-21
139
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                                                                                                                                      Scoring table:
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Perfect score:
                                            OM protein -
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                                                                                                                    Sequence:
                                                                                                                                                                 Searched:
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No.
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           Sequence 1078, Ap
Sequence 15, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 2, Appli
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-09-404-108-4
; Sequence 4, Application US/09404108
; Patent No. 6590077
; GENERAL INFORMATION:
APPLICANT Tang, Tom
; APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Profile C.
APPLICANT: WITHEN THE APPLICATION WIMBER: US/09/404,108
CURRENT APPLICATION WIMBER: US/09/404,108
CURRENT FILING DATE: 1990-09-23
BEALIER FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL PROGram
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                      US-09-172-977-4

i Sequence 4, Application US/09172977

i Sequence 4, Application US/09172977

j Patent No. 598963

i GENERAL INFORMATION:

j APPLICANT: Tang, Y. Tom

j APPLICANT: Guegler, Karl J.

APPLICANT: Groley, Neil C.

j APLICANT: Yue, Henry, Y. Hinkan ANKYRIN FAMILY PROTEIN

FILE REFRENCE: PF-0615 US

CURRENT APPLICATION NUMBER: US/09/172,977

CURRENT APPLICATION NUMBER: 1998-10-14

j KOURRENT FILING DATE: 1998-10-14

j SEQ ID NO 4

j SEQ ID NO 4

j SEQ ID NO 6

much Application NUMBER PRESENTED NO 6

j CURRENT APPLICATION NUMBER PROTEIN

j CURRENT PLING DATE: 1998-10-14

j SEQ ID NO 6

j LENGTH: 1839
                       US-09-082-279B-1078
US-09-315-364B-1078
US-09-314-784B-1078
US-09-518-965A-1078
US-09-543-641A-1078
US-09-543-641A-1078
US-09-255-96A-15
US-09-270-751-33
US-09-031-485-2
US-08-47-429A-2
US-09-655-474-2
US-09-655-474-2
US-09-655-474-2
US-09-655-474-2
US-09-655-474-2
US-09-655-474-2
US-08-84-161A-3
US-09-65-474-2
US-09-65-474-2
US-09-65-474-2
US-08-84-161A-4
US-08-84-161A-4
                                                                                                                                                                                                                                                                                               ALIGNMENTS
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Best Local Similarity 96.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
GRANISM: Homo sapiens
FRATURE:
OTHER INFORMATION: 929491
US-09-172-977-4
1449
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US-08-519-103-18
Sequence 18, Application US/08519103
Patent No. 2533730
GENERAL INFORMATION:
APPLICANT: deLange, Titia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
                                                                                                                                 Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 835
TYPE: PRI
                                                                          CRGANISM: Carassius auratus US-09-619-353-7
                                                                                                                                                                                                                                                   199 LAYIVKHLGWSW 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.7'
Matches 11; Conservative
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STRANDEDNESS: si
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; Sequence 1246, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loi,
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT APPLICATION NUMBER: 60/127,352
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR PILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1246
; TYPE: PRI
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88.5%; Score 123; DB 4; Length 3924;
Best Local Similarity 96.0%; Pred. No. 1.5e-09;
Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                     Length 1839;
                                                                                                                                                                            1; Indels
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Pred. No. 6.4e-10;
0; Mismatches 1;
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APPLICANT: Speca, David J.
APPLICANT: Lin, David M.
APPLICANT: Lin, David M.
APPLICANT: Lin, David M.
APPLICANT: Dittman, Andrew H.
APPLICANT: Fan, Jinhong
TITLE OF INVENTION: Odorant Receptors
FILE REFRENCE: B99-038-2
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/144,766
PRIOR, FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                       1449 ERIEERLAYIADHLGFSWTELAREL 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3534 ERIEERLAYIADHLGFSWTELAREL 3558
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Patent No. 6410249
GENERAL INFORMATION:
                                                                                                                                     Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative (
                    TYPE: PRT
CRGANISM: Homo sapiens
FEATURE:
CHER INFORMATION: 929491
US-09-404-108-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-538-092-1246
      LENGTH: 1839
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US-08-519-103-16
US-08-519-103-16

Sequence 16, Application US/08519103

Patent No. 5733730

GENERAL INFORMATION:
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.6%; Score 49.5; DB 1; Length 51; 40.7%; Pred. No. 1.6; tive 4; Mismatches 11; Indels
Score 52; DB 4; Length 835;
Pred. No. 15;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUFTWARE: Patentin Release #1.0, Version #1.30 CARRENT APPLICATION DATA: PILING DATE: 25-AUG-1995
CLASSIFICATION: 435
TTORNEY: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |:|:| | | |:|:| WTEEEDRIIYEAHKRLGNRWAEIAKLL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E.
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                   1 WERIEERLAYIA-DHLGFSWTELARAL 26
                                                                                                                                                                                                                                                                                                                                                      6 WTEEEDRIIYEAHKRLGNRWABIAKLL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA ZIP: 076"
   NAME: David A. Jackson
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
RELECOMMUNICATION INFORMATION:
TELEFONE: 201-487-5800
TELEFAX: 201343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DAVIG A. Jackson
REGISTRATION NUMBER: 26,742
REPENCE/DOCKET UNDRER: 600-:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201-343-1684
                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                 TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-09-018-635-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIRANDEDNESS: BIT
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Matches 11; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF WINDER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESSE: KLAUBER & JACKSON STREET: 411 Hackensack Avenue STREET: 414 Hackensack STREET: 1 Hackensack STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.6%; Score 49.5; DB 1; Length 51; 40.7%; Pred. No. 1.6; tive 4; Mismatches 11; Indels
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPATER: PER PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATE: US/08/519,103
FILING DATE: 25-AUG-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WERIEERLAYIA-DHLGFSWTELARAL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 WTEEEDRIIYQAHKRLGNRWAEIAKLL 32
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: CRANGE-FEULY, SHAKON E.
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 600-1-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.73
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-519-103-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                STATE: New COUNTRY: US ZIP: 07601
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US-09-018-635-16
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Gaps
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Patent No. 6297356
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Broccoll, Dominique
APPLICANT: Smogorzewska, Agata
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.6%; Score 49.5; DB 3; Length 51; 40.7%; Pred. No. 1.6;
  DB 3; Length 51;
                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,635
Query Match
35.6%; Score 49.5; Di
Best Local Similarity 40.7%; Pred. No. 1.6;
Matches 11; Conservative 4; Mismatches
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ADDRESSEE: KLAUBER & JACKSON
CORRESPONDENCE ADDRESS
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CLASSIFICATION: 435
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Sequence 18, Application US/09912962
Patent No. 6586577
GENERAL INFORMATION:
GENERAL INFORMATION:
Broccoli, Dominique
Smogorzewska, Agata
TITLE OF INVENTION: TELLOMERE REPEAR BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                        APPLICANT: de Lange, Titia
Broccoli, Dominique
Smogorzewska, Agata
TITLE OF INVENTION: TELCMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.6%; Score 49.5; DB 4; Length 51; 40.7%; Pred. No. 1.6; Live 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/912,962
FILING DATE: 29-701-2001
CLASSIFICATION: <1001
CLASSIFICATION AND ATA:

APPLICATION DATA:

APPLICATION NUMBER: 09/018,635
FILING DATA:

NAME: DATIG A. Jackson
REFERENCE/DOCKET NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-142 CIP1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-912-962-16
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                              6 WTEEEDRIIYQAHKRLGNRWAEIAKLL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WERIEERLAYIA-DHLGFSWTELARAL 26
  1 WERIEERLAYIA-DHLGFSWTELARAL 26
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON STREET: 411 Hackensack Avenue CITX: Hackensack STATE: New Jersey COUNTRY: USA
                                                                                                                                US-09-912-962-16; Sequence 16, Application US/09912962; Sequence 16, Application US/09912962; Pattent No. 6586577; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 51 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 40.74
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-09-912-962-18
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Gaps
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                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/912,962

FILING DATA:

APPLICATION NUMBER: 09/018,635

FILING DATA:

APPLICATION NUMBER: 09/018,635

ATORNEY/AGENT INFORMATION:

NAME: David A. Jackson

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-142 CIP1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08928941D
; Sequence 4, Application US/08928941D
; Patent No. 6180763;
densral INFORMATION:
APPLICANT: Hirai, Hiroshi
APPLICANT: Charles
; TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
; TITLE OF INVENTION: THEREOF
; TITLE OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
ADDRESSEE: David A. Jackson, Esq.
STREET: Floor
STREET: Floor
CITY: Hackensack Ave, Continental Plaza, 4th
STREET: New Jersey
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,941D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
35.6%; Score 49.5; Di
Best Local Similarity 40.7%; Pred. No. 1.6;
Matches 11; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: innear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-912-962-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WERIEERLAYIA-DHLGFSWTELARAL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 WTEEEDRIIYQAHKRLGNRWAEIAKLL 32
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-343-1684
                                                 STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Gallus gallus
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US-08-928-941D-36
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US-09-280-590A-46
ORGANISM:
                                                                                                                                                                                                                                              RESULT 13
US-09-280-590A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-08-928-941D-36
| Sequence 36, Application US/08928941D|
| Patent No. 6180763|
| GENERAL INFORMATION:
| APPLICANT: Hirai, Hiroshi|
| APPLICANT: Sherr, Charles|
| TITLE OF INVENTION: THEREOF|
| NUMBER OF SEQUENCES: 36
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: David A. Jackson, Esq.
| STREET: 411 ackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTEY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLEM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,941D
                                                            1340-1-002 N CIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bsq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-
TELECOMMUNICATION INFORMATION:
               NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-
TELECOMUNICATION INFORMATION:
TELEPA: 201-487-5800
TELEPA: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
STRANDENNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPXX: 201-343-1684
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus US-08-928-941D-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
FRACMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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Gaps
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35.6%; Score 49.5; DB 3; Length 156;
Best Local Similarity 40.7%; Pred. No. 5.6;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esg.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bother, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
THEREOF
                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,590A
FILING DATE: 29-Mar-1999
CLASSIFICATION: <unhain-unit of the company of the company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Bsq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 201-487-5800
TELEPRA: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 40.7%; Pred. No. 5.6;
Matches 11; Conservative 4; Mismatches 11;
                                                                                                                                                                                                                                                                             110 WIEEEDRIIYQAHKRLGNRWAEIAKLL 136
                                                                                                                                                                                                                      1 WERIEERLAYIA-DHLGFSWTELARAL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WERIEERLAYIA-DHLGFSWTELARAL 26
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TYPE: amino acid
STRANDEDDESS: clnknown>
TOPOLOGY: linear
MOLECTLE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09280590A; Patent No. 6303772; GENERAL INFORMATION: APPLICANT: Hirai, Hiroshi Sherr, Charles Inoue, Kazushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
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35.6%; Score 49.5; DB 3; Length 156;
Best Local Similarity 40.7%; Pred. No. 5.6;
Matches 11; Conservative 4; Mismatches 11; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUW TEPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,590A
FILING DATE: 29-Mar-1999
CLASSIFFICATION: <UNANOWN-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                               Bodner, Sarah M.
IITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bodner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALOCKALI, AGEN LEGG., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION INPORMATION:
TELEPHONE: 201-487-5800
TELEPAK: 201-343-1684
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES
FRAGMENT TYPE: «Unknown»

ORIGINAL SOURCE:

GRANISM: Gallus gallus

SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-280-590A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 WTEEEDRIIYQAHKRLGNRWAEIAKLL 136
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Sequence 46, Application US/09280590A
Patent No. 6303772
GENERAL INFORMATION:
APPLICANT: Hirai, Hiroshi
Sherr, Charles
Inoue, Kazushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09892398
Patent No. 6673902
GENERAL INFORMATION:
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Sherr, Charles
Inoue, Kazushi
                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                     Floor
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COMPTRY: Backensack
STATE: New Jersey
COMPTRY: USA
COMPTRY: USA
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COMPTRY: LOW Group tible
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COMPTRY: LOW FOOD disk
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November 10, 2004, 15:53:52; Search time 25.0772 Seconds (without alignments) 366.225 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                   Run on:
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US-10-092-750-21 139 1 WERIEERLAYIADHLGFSWTELARAL 26 Title: Perfect score: Sequence:

1566620 seqs, 353225886 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: \cgn2 \(\) \cgn2 \(\

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 21, Appl	Sequence 1, Appli	Sequence 229829,	Sequence 2, Appli	Sequence 2995, Ap	Sequence 117, App	Sequence 45, Appl	Sequence 128, App	Sequence 87, Appl			Sequence 45, Appl	Sequence 124, App
QI	US-10-092-750-21	US-10-336-031-1	US-10-425-115-229829	US-10-336-031-2	US-10-104-047-2995	US-10-205-194-117	US-10-334-143-45	US-09-972-211-128	US-10-087-684-87	US-10-218-779-87	US-10-096-625-128	US-09-970-944-45	US-10-037-417-124
	14	14	17	14	14	14	15	11	15	15	15	10	12
Query Match Length DB	26	396	253	294	400	1762	3913	95	95	95	95	96	96
Query	100.0	88.5	90.6	64.7	64.7	64.7	64.7	41.4	41.4	41.4	41.4	41.4	41.4
Score	139	123	112	06	90	90	90	57.5	57.5	57.5	57.5	57.5	57.5
Result No.	-	CVI	e	4	ιΩ	9	7	œ	თ	10	11	12	13

Sequence 9326, Ap Sequence 7, Appli Sequence 9645, Ap Sequence 7619, Ap Sequence 7619, Ap	4 6 8 4 4	ednence ednence ednence ednence ednence	Sequence 6548, Ap Sequence 9923, Ap Sequence 167029, Sequence 17817, A Sequence 11, Appl Sequence 26724, Sequence 33, Appl	sednence Sednence Sednence Sednence Sednence
4 US-10-156-7 4 US-10-151-2 7 US-10-739-9 4 US-10-156-7	US-10-369-493-4065 US-09-912-962-16 US-09-912-962-18 US-09-912-962-18 US-09-892-398-46	4 US-10-321-857-24 4 US-10-318-675-24 4 US-10-156-761-11 4 US-10-146-473-77 6 US-10-424-599-16	4 US-10-36-493-654 4 US-10-156-761-992 6 US-10-437-963-167 5 US-10-282-1228-77 5 US-10-808-0318-11 5 US-10-424-599-267 12-0-808-0318-11 13-0-808-0318-11	-808-031A-6 -808-031A-6 -808-031A-4 -808-031A-2 -808-031A-2 -351-641-1 -767-701-3 0-021-811-6
4.10.00.00 t	200000) 44 44 40 W W	8407824	4 4 2 2 4 4 4 2 2 4 4 4 4 4 4 4 4 4 4 4
5 37.		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	88888 C C C C C C C C C C C C C C C C C	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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ALIGNMENTS

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Gaps
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               Sequence 21, Application US/10092750;
Sequence 21, Application US/10092750;
Publication No. US20030032157A1;
GENERAL INPORMATION;
APPLICANT: Hammond, Philip W.
APPLICANT: HAMPIN, Julia
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1;
FILE REFERENCE: 50036/050002;
CURRENT APPLICATION NUMBER: US/10/092,750;
CURRENT APPLICATION NUMBER: US/20/274,526
NUMBER OF SEQ ID NOS: 253
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 26
TYPE: PRI
CRANTESM: Homo sapiens
US-10-092-750-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 139; DB 14; Best Local Similarity 100.0%; Pred. No. 3.6e-13; Matches 26; Conservative 0; Mismatches 0;
US-10-092-750-21
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; Sequence 1, Application US/10336031; Publication No. US20030167491A1; GENERAL INFORMATION: RESULT 2 US-10-336-031-1

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SEQ ID NO 117
LENGTH: 1762
TYPE: PR:
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-205-194-117
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 229829
LENGTH: 253
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               APPLICANT: GRAMOLINI, ANTHONY O.
APPLICANT: MOHLER, PETER J.
TITLE OF INVENTION: METHODS OF MODULATING LOCALIZATION AND PHYSIOLOGICAL
TITLE OF INVENTION: FUNCTION OF 1P3 RECEPTORS
FILE REFERENCE: 1579-777
CURRENT APPLICATION NUMBER: US/10/336,031
CURRENT FILING DATE: 2003-01-03
PRIOR PILING DATE: 2002-01-03
PRIOR FILING DATE: 2002-01-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VEF. 2.1
SEQ ID NO 1
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Sequence 2, Application US/10336031
Publication No. US2030167491A1
Publication No. US2030167491A1
SEMERAL INFORMATION:
APPLICANT: BENNETT, VANN
APPLICANT: GRAMOLINI, ANTHONY O.
APPLICANT: MOHLER, PETER J.
TITLE OF INVENTION: METHODS OF MODULATING LOCALIZATION AND PHYSIOLOGICAL
TITLE OF INVENTION: FUNCTION OF IP3 RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_141200C.1.pep
US-10-425-115-229829
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 123; DB 14;
Pred. No. 1.5e-09;
0; Mismatches 1;
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NAME/KEX: unsure
LOCATION: (1). (253)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040214272A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 ERMEERLAYIADHLGFSWTELA 253
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 88.5%;
Best Local Similarity 96.0%;
Matches 24; Conservative
APPLICANT: BENNETT, VANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus sp. US-10-336-031-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -10-425-115-229829
                                                                                                                                                                                                                                                                                                          LENGTH: 396
TYPE: PRT
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APPLICANT: Warner-Lambert Company
APPLICANT: Dixon, Alistair
APPLICANT: Dixon, Alistair
APPLICANT: Dixon, Alistair
APPLICANT: Brooksbank, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REPRENCE: WL-A-018210
CUBRENT APPLICATION NUMBER: US/10/205,194
CUBRENT APPLICATION NUMBER: GB 0118354.0
PRIOR APPLICATION NUMBER: GB 0118354.0
NUMBER OF SEQ ID NOS: 177
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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US-10-104-047-2995
US-10-104-047-2995
Sequence 2995, Application US/10104047
Publication No. US20030236392A1
GENERAL INPORMATION:
TIPLE OF INVENTION: No. US20030236392A1e1
SPIOR PELING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTION OF T. 2.1
SEQ ID NO 2995
                                                                                                                                                                                                                                                                                                                            Query Match 64.7%; Score 90; DB 14; Length 294; Best Local Similarity 68.0%; Pred. No. 7.4e-05; Matches 17; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 90; DB 14; Length 400;
Pred. No. 0.0001;
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FILE REFERENCE: 1579-777
CURRENT APPLICATION NUMBER: US/10/336,031
CURRENT FILING DATE: 2003-01-03
PRICE PELICATION NUMBER: 60/344,047
PRICE FILING DATE: 2002-01-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VET: 2.1
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ERIEERLAYIADHLGFSWTELARAL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 ERTDIRMAIVADHLGLSWTELAREL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 ERTDIRMAIVADHLGLSWTELAREL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ERIBERLAYIADHLGFSWTELARAL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117, Application US/10205194 Publication No. US20030134301A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-10-104-047-2995
                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mus sp.
US-10-336-031-2
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Query Match 41.4%; Score 57.5; DB 11; Length 95; Best Local Similarity 53.8%; Pred. No. 1.2; Matches 14; Conservative 2; Mismatches 9; Indels
      CURRENT APPLICATION NUMBER: US/09/972,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ERIBERLAYIADH-LGFSWTELARAL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 ELTREKLAKLICHDIGDDWRELARKL 34
                           CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/238,325
PRIOR FILING DATE: 2000-10-05
PRIOR PELICATION NUMBER: 60/238,323
PRIOR FILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PELICATION NUMBER: 60/238,400
PRIOR PILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,401
PRIOR PILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,402
PRIOR PILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,339
PRIOR PILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,339
PRIOR PILING DATE: 2000-10-06
PRIOR PELING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,383
PRIOR PILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,383
PRIOR PILING DATE: 2000-10-06
PRIOR PELING DATE: 2001-0-06
PRIOR APPLICATION NUMBER: 60/236,860
PRIOR PELING DATE: 2001-0-06
PRIOR PILING DATE: 2001-0-06
PRIOR PELING DATE: 2001-0-06
PRIOR PELING DATE: 2001-0-06
PRIOR PILING DATE: 2001-0-0-06
PRIO
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Publication No. US20040029116A1
GAPBLICANT: Edinger, Shlomit R.
APPLICANT: MacDougall, John R.
APPLICANT: Miller, Isabelle
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Grosse, William M.
APPLICANT: Eleger, Daniel K.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Cathereine E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Boldgy, Ferenc L.
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Padigur, Muralidhara
Mishra, Vishnu
Shenoy, Suresh G.
Rastelli, Luc
Tchernev, Velizar T.
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-972-211-128
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US-10-334-143-45

Sequence 45, Application US/10334143

Sequence 45, Application US/10334143

Publication No. US20040009549A1

GENERAL INFORMATION:

APPLICANT: GUDGRIEV, IGOR VYACHESLAVOVICH

APPLICANT: SUDARSAMAM, SUCHA

TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD

TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD

CURRENT FILING DATE: 2002-12-31

CURRENT FILING DATE: 2001-12-31

NUMBER OF SEQ ID NOS: 207

SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                             Query Match 64.7%; Score 90; DB 14; Length 1762; Best Local Similarity 68.0%; Pred. No. 0.00052; Matches 17; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 64.7%; Score 90; DB 15; Length 3913; Best Local Similarity 68.0%; Pred. No. 0.0012; Matches 17; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                 1474 ERTDIRMAIVADHLGLSWTELAREL 1498
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                                                                                                                                                                                                                                                           2 ERIBERLAYIADHLGFSWTELARAL 26
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Publication No. US20040048245A1
GENERAL INFORMATION:
; FEATURE:
; OTHER INFORMATION: Ankyrin isoform
US-10-205-194-117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-334-143-45
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US-09-972-211-128
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LENGTH: 3913
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APPLICANT: Ji, Weizhen
TITLE OF INVENTION: No. US20040068095Alel Human Proteins, Polynucleotides Encoding The
TITLE OF INVENTION: Methods of Using The Same
FILE REFERENCE: 21402-141 CIP
CURRENT APPLICATION NUMBER: US/10/096,625
CURRENT FILING DATE: 2000-03-13
PRIOR FILING DATE: 2001-10-05
PRIOR PLING DATE: 2000-10-05
PRIOR PLING DATE: 2000-10-05
PRIOR PLING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 95;
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Best Local Similarity 53.8%; Pred. No. 1.2;
Matches 14; Conservative 2; Mismatches
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        CURRENT FILING DATE: 2002-08-14
PRIOR PEDICACHON NUMBER: 60/253,834
PRIOR PEDICATION NUMBER: 60/250,-926
PRIOR APPLICATION NUMBER: 60/260,-926
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR PILING DATE: 2001-08-20
PRIOR PILING DATE: 2001-08-20
PRIOR PILING DATE: 2001-08-20
PRIOR PILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PATCHIN VET: 2.1
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5. US20040068095A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Taupier Jr. Raymond J
APPLICANT: Burgess, Catherine E
APPLICANT: Bertall: Bryan D
APPLICANT: Restell:, Luca
APPLICANT: Rattell:, Luca
APPLICANT: Alsobrok II, John P
APPLICANT: Alsobrok II, John P
APPLICANT: Alsobrok II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Lepley, Denise M
APPLICANT: Lepley, Miliam M
APPLICANT: Lepley, Benise M
APPLICANT: Spytek, Kimberly Ann
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Smithson, Glennda
Szekeres Jr, Edward S
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Gerlach, Valerie
Ellerman, Karen
MacDougall, John R
Gunther, Erik
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Homo sapiens
US-10-218-779-87
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Publication No. US20
GENERAL INFORMATION:
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US-10-096-625-128
                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 87
LENGTH: 95
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APPLICANT:
APPLICANT:
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APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Gangolli, Esha A.
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 2140-214 CIP
CURRENT APPLICATION NUMBER: US/10/087,684
CURRENT FILING DATE: 2003-03-10.
PRIOR APPLICATION NUMBER: 60/253,834
PRIOR APPLICATION NUMBER: 60/250,926
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR PELING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/274,194
PRIOR APPLICATION NUMBER: 60/274,194
PRIOR PELING DATE: 2001-03-08
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/327,456
PRIOR PELING DATE: 2001-08-20
PRIOR PELING DATE: 2001-08-20
PRIOR CONTUMBER: CURSEQLIST VETSION 0.1
SEQ ID NOS: 220
LENGGH: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artifical Sequence: Domain US-10-087-684-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 95;
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PPLICANT: Gangolli, Esha
ITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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53.8%; Pred. No. 1.2;
tive 2; Mismatches 9;
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CURRENT APPLICATION NUMBER: US/10/218,779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 87, Application US/10218779 Publication No. US20040029222A1 GENERAL INFORMATION:
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adigaru, Muralidhara
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Alsobrook II, John
Lepley, Denise
Rieger, Daniel
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Casman, Stacie
Spytek, Kimberly
Boldog, Ferenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mishra, Vishnu
Patturajan, Meera
Shenoy, Suresh
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Rastelli, Luca
Tchernev, Velizar
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Malyankar, Uriel
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Edinger, Shlomit
APPLICANT: MacDougall, John
APPLICANT: Millet, Isabelle
APPLICANT: Elleramn, Karen
APPLICANT: Stone, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.88
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vernet, Corine
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OTHER INFORMATION: Description of Artificial Sequence: DEATH domain
OTHER INFORMATION: Consensus Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Taupier úr, Raymond ú
APPLICANT: Miller, Charles E
APPLICANT: Bisen, Andrew ú
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 21402-235

CURRENT APPLICATION NUMBER: US/10/037,417

CURRENT FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: 60/260,018

PRIOR PRICHAIDN NUMBER: 60/260,360

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-08

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-03-02

PRIOR PILING DATE: 2001-03-02

PRIOR PILING DATE: 2001-05-15

PRIOR PILING DATE: 2001-05-15

PRIOR PILING DATE: 2001-05-15

PRIOR PILING DATE: 2001-05-15

PRIOR PILING DATE: 2001-07-12

PRIOR PILING DATE: 2001-09-10

PRIOR PILING DATE: 2001-09-10

PRIOR PILING DATE: 2001-09-10

PRIOR PILING DATE: 2001-09-11

PRIOR PILING DATE: 2001-09-12

PRIOR PILING DATE: 2001-09-13

PRIOR PILING DATE: 2001-09-13
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                                   Kekuda, Ramesh
Alsobrook II, John P
Tchernev, Velizar T
Liu, Kiachong
Spytek, Kimberly A
Patturajan, Mera
Grosse, William M
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson, David W
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                      Burgess, Catherine E
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                               Li, Li
Gorman, Linda
Edinger, Shlomit R
Sciore, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ellerman, Karen
Malyankar, Uriel M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rothenberg, Mark
Stone, David J
Boldog, Ferenc L
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shenoy, Suresh G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-156-761-9326
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US-09-970-944-45
| US-09-970-944-45
| Gequence 45, Application US/09970944
| Publication No. US20330204052A1
| GENERAL INPORMATION:
| APPLICANT: Herrman, John L
| APPLICANT: Rastelli, Luca |
| APPLICANT: Rastelli, Luca |
| TITLE OF INVENTION: Antibodies Directed Against these Proteins |
| TITLE OF INVENTION: Antibodies Directed Against these Proteins |
| FILE REFERENT APPLICATION NUMBER: US/09/970,944
| CURRENT APPLICATION NUMBER: 06/237,862 |
| FRIOR APPLICATION NUMBER: 60/237,862 |
| FRIOR FILING DATE: 2000-10-04 |
| NUMBER OF SEQ ID NOS: 62 |
| SOFTWARE: Patentin Ver. 2.1 |
| SOFTWARE: Patentin Ver. 2.1 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
41.4%; Score 57.5; DB 15; Length 95;
Best Local Similarity 53.8%; Pred. No. 1.2;
Matches 14; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 41.4%; Score 57.5; DB 10; Length 96; Best Local Similarity 53.8%; Pred. No. 1.2; Matches 14; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ERIEERLAYIADH-LGFSWTELARAL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 ELTREKLAKLLDHDLGDDWRELARKL 34
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RESULT 13
US-10-037-417-124
Sequence 124, Application US/10037417
Publication No. US20040052806A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-096-625-128
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40.3%; Score 56; DB 14; Length 384;
Best Local Similarity 48.0%; Pred. No. 9.3;
Matches 12; Conservative 1; Mismatches 12; Indels
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Pred. No. 83;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gegener 7. Application US/10151208
| Publication No. US20030105285A1
| GENERAL INFORMATION:
| APPLICANT: Ngai, John
| APPLICANT: Speca, David M.
| APPLICANT: Isaccff, Elmid Y.
| APPLICANT: Isaccff, Elmid Y.
| APPLICANT: Dittman, Andrew H.
| APPLICANT: Dittman, Andrew H.
| APPLICANT: Pan, Jinhong
| TILLE OF INVENTION: Odorant Receptors
| FILE REFERENCE: B99-038-2
| CURRENT APPLICATION NUMBER: US/10/151,208
| CURRENT APPLICATION NUMBER: US/09/619,353
| PRIOR FILING DATE: 2000-07-19
| PRIOR FILING DATE: 1999-07-20
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: PatentIn Ver. 2.1
| SENOTURENT H35
GENERAL INFORMATION:
APPLICANT: CMURA, SATCSHI
APPLICANT: IKEBA, HARUO
APPLICANT: ISHIKAWA, UNN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
SEQ ID NO 9326
LENGTH: 384
LENGTH: 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 WHRTEERAAQALDHIGLAGRAEPRA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; CARASSIUS AUTATUS; ORGANISM: Carassius auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 LAYIVKHLGWSW 210
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Search completed: November 10, 2004, 16:36:05 Job time : 26.0772 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2004, 11:36:51 ; Search time 5.25617 Seconds
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Run on: November 10, 2004, 11:36:51; Search time 5.25617 Seconds (without alignments)
475.942 Million cell updates/sec Title: US-10-092-750-21
Perfect score: 139
Sequence: 1 WERIEBERLAYIADHLGFSWTELARAL 26
Scoring table: BLOSUM62

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283416 segs, 96216763 residues Total number of hits satisfying chosen parameters: 283

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 79:*
1: Dir1:*
2: Dir2:*
3: Pir3:*
4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	scription	107	'n	m	m	m	3	erythro			'n	٦,	4	무	Α,	g	tran	probable transport	hypothetical prote	₽	. transforming prote									prot
SOUTHERNES	Ω	S37431	T42714	T42715	T42713	T42716	A55575	S37773	S37771	149502	B35049	A35049	SUHUK	F69820	T36100	C64935	E90936	A85785	B64481	T00077	I50667	870090	T36359	S11198	QOYV	TVMSMB	A55073	TVMSMY	I49497	803423
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	ength	924	9	94	94	96	7	138	84	9	85	ø	ø	311	æ	σ	O,	σ	484	ч	S	ч	S	4	α	3	4	М	S	IU.
ф	Query Match	88		4.	4.	64.7	64.7	59.0	φ.	59.0	4	4.	54.7	41.0	37.4	37.4	37.4	۲.	36.7	ġ	ė.	è.	ιņ.	ů.	'n.	35.6	ď.	'n.		S.
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	ult No.	-	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

transforming prote	transforming prote	probable dATP pyro	probable maltose-b	hypothetical prote	transforming prote	transcription fact	chitinase (EC 3.2.	hypothetical prote	phosphate acetyltr	probable reverse g	conserved hypothet	RNA-directed DNA p	RNA-directed DNA p	chitinase (EC 3.2]	probable sugar tra
TVCHM	TVHUMB	AF0250	T03553	S01085	836095	A47212	S04856	T24668	AE0313	C71129	F69370	A42383	RRYC62	S52422	AF0117
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_	-	47	137	294	728	660	499	988	717	624	176	480	485	499	499
76	76	Н	7	H		~				-		•			
35.6 76				35.3											
49.5 35.6 76						34.9				34.2					

ALIGNMENTS

	RESULT 1
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	ankytin 2, meuronal Loig Splice torm - numan Naltarnata names ankytin R. 440K smlite form: ankytin R. brain ankytin: non-arythroid ;
	540
	C;Species: Homo sapiens (man) C;Date: (A.Tarilook Hearmanne ravision (6.Tarilook Htawt channe (6.Tarilook)
	R,Chan, W.
	submitted to the EMBL Data Library, September 1993 3.Deference mumber. 637431
	A. A. Caccaston and a second an
	A;Status: preliminary
	A;Molecule type: MRNA - Popes Anne: 1=1004 / CHIA
	A. COSB-references: UNIPROT: Q01484; EMBL: 226634; NID: 9406287; PIDN: CAA81387.1; PID: 940628
	o. Cell biol. 114, 241-225, 1991 J. Title I Isolation and characterization of CDNAs encoding human brain ankvrins reveal a f
	oding maman prain and ring recar
	A/Status: preliminary
	A; Molecule type: mRNA
	A:Cross-terercos: GB:X56957
	AAACCESSION: E35943
	Ajoracus: pretiminary b.McTerile tyme: mbnk
	7.700.000.000.000.000.000.000.000.000.0
	A.Cross-references: EMBL: X56958
	RiTse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,
	A/Title: Isolation and chromesomal localization of a novel nonerythroid ankyrin gene.
	Ajratateine immuda: Atolot; Mold.yzoobal; Fild.tolotoo A.bromesejone barotta
	A Molecule type: DNA
	A;Residues: 463-474,'PE',477-495 <tse></tse>
	A,Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
	R; Chan, W.; Kordell, E.; Bennett, V.
	V. CELL BIOL. 125, 1485-1443, 1594 N. Titll. 440. Mr and consists of the major design manually recuilated demain and eal
	A:TREFERS number: A49462: MIID:94075409: PMID:825844
	A;Accession: A49462
	A;Status: preliminary; nucleic acid sequence not shown
	A; Molecule types, mRNA
	Afresiumes: 1-5244 KESS> Afresiumes: 1-5244 KESS> Afresiumes: TRME: 755634 NID-4406987 DIDN-62881387 1 DID-440698
	Control of the contro
	A,Gene: GDB:ANK2
	A;Cross-references: GDB:127607; OMIM:106410
	A; Map position: 455-4925.
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265-297/Domain: ankyrin repeat 298-330/Domain: ankyrin repeat

repeat

ankyrin

repeat

repeat repeat repeat repeat

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repeat

:595-627/Domain: ;628-660/Domain: ;661-693/Domain: F;694-726/Domain: F;727-759/Domain: F;760-792/Domain:

562-594/Domain:

repeat

repeat repeat

ankyrin ankyrin ankyrin

repeat

ankyrin

331-363/Domain: /Domain: 397-429/Domain: :430-462/Domain: /Domain: 496-528/Domain: Domain:

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ankyrin 3, splice form 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42716
R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
                         C,Accession: T42715
R,Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L. J. Cell Biol. 130, 313-330, 1995
A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Description: supposed to play an important role in the polarized distribution of many i A,Note: major kidney ankyrin
C,Superfamily: ankyrin, ankyrin repeat homology
C,Keywords: alternative splicing
                                                                                                                                                                                                                                           A;Residues: 1-1940 <PET>
A;Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604.
A;Experimental source: strain C57BL/6J; kidney
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C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1940;
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68.0%; Pred. No. 0.00021;
iive 3; Mismatches 5; Indels
                                                                                                                                                 A,Reference number: Z22237; MUID:95340633; PMID:7615634
A,Accession: T42715
                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA__
                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 10
A;Introns: 834/1
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keyworda: alternative splicing
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Best Local Similarity 68.04
Matches 17; Conservative
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nes 17; Conservative
                                                                                                                                    the repeat domain.
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C; Function:
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                                                                                                                                                                                                                                                                                                                                                      A;Gene: Ank3
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A;Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710551; PIDN:AAB01605
A;Experimental source: strain C57BL/6J; kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ankyrin 3, splice form 2 - mouse
C,Species: Mus musculus (house mouse)
C,Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42714
K;Peters, L.L., John, K.M.; Lu, F.M.; Bicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.
J. Cell Biol. 130, 313-330, 1995
A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
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            C;Keywords: alternative splicing
F;2-3924/broduct: ankyrin 2, long form #status predicted <MAT>
F;2-1443,3585-3924/broduct: ankyrin 2, short form #status predicted <MA2>
F;2-1443,385-3924/broduct: ankyrin 2, short form #status predicted <MA2>
F;63-95/Domain: ankyrin repeat homology <AN02>
F;129-161/Domain: ankyrin repeat homology <AN03>
F;162-190/Domain: ankyrin repeat homology <AN05>
F;191-223/Domain: ankyrin repeat homology <AN05>
F;232-264/Domain: ankyrin repeat homology <AN06>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 8.8e-09;
0; Mismatches 1; Indels C
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Best Local Similarity 68.0%; Pred, No. 0.00019;
Matches 17; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reference number: Z22237; MUID:95340633; PMID:7615634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Status: preliminary; translated from GB/EMBL/DDBJ;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                      <AN11>
                                                                                                                                                                                                                                                           < ANO 8 >
                                                                                                                                                                                                                                                                                     < ANO 9 >
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A,Introns: 1587/1
C,Superfamily: ankyzin; ankyzin repeat homology
C,Keryaords: alternative splicing
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C;Species: Mus musculus (house mouse)
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88.5%; ilarity 96.0%; Conservative

Query Match Best Local Similarity Matches 24, Conser

8 셤 the repeat domain.

A;Gene: Ank3 C;Genetics:

Best Loca Matches

RESULT 3

g

repeat repeat

ankyrin ankyrin

F;793-825/Domain: ankyrin

repeat

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Subjections: Muse musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C.Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C.Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C.Bacesion: 837771
S.Biol. Chem. 268, 9533-9540, 1993
A.Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found amm.
A.Accession: 837771; MUD: 93252825; PMID: 8486643
A.Accession: 837771; MUD: 93252825; PMID: 8311816; PIDN: CAA48801.1; PID: 931181
A.Accession: 837771; Multiple 5' and 3' ends are found amm.
A.Accession: 837771; Multiple 5' and 3' ends are found amm.
A.Accession: 837771; Multiple 5' AM01-87; AM01-87;
                                                                                                                                                                                                                                                                                                                      ankyrin, erythrocyte - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 27-May-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S37773
R;Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
J; Biol. Chem. 266, 9533-9540, 1993
A;Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found amc A;Reference number: S37771; MUID:93252825; PMID:8486643
A;Accession: S37773
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                                                                                                     4088 ERTDIRMAIVADHLGLSWTELAREL 4112
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                                                                   2 ERIEERLAYIADHLGFSWTELARAL 26
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Best Local Similarity 60.0
Matches 15; Conservative
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A/Status: preliminary
A/Status: mRNA
A/COSS-references: UNIPROT:Q12955; GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025
A/Gene: GDB:ANK3
A/COSS-references: GDB:424503; OMIM:600465
A/Map position: 10q21-10q21
C/Superimanily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C/Keywords: alternative splicing; peripheral membrane protein
F/73-105/Domain: ankyrin repeat homology <AN01>
A; Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.

A; Reference number: Z22237; MUID:95340633; PMID:7615634

A; Accession: T42716

A; Accession: T42716

A; Residues: preliminary; translated from GB/EWBL/DDBJ

A; Residues: 1-1961 <PET>
A; Residues: 1-1961 <PET>
A; Residues: 1-1961 <PET>
A; Experimental source: strain C57BL/6J; kidney

A; Experimental source: strain C57BL/6J; kidney
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Pred. No. 0.00021;
3; Mismatches 5; Indels
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A;Map position: 10
C;Superfamily: ankyrin; ankyrin repeat homology
C;Ksuperfamily: anternative splicing
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F)139-171/Domain: ankyrin repeat homology
F)201-233/Domain: ankyrin repeat homology
F)201-233/Domain: ankyrin repeat homology
F)234-266/Domain: ankyrin repeat homology
F)267-299/Domain: ankyrin repeat homology
F)300-332/Domain: ankyrin repeat homology
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larity 68.0%;
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F)366-398/Domain: ankyrin repeat
F)399-431/Domain: ankyrin repeat
F)32-464/Domain: ankyrin repeat
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F;729-76/Domain: ankyrin repeat
F;765-794/Domain: ankyrin repeat
F;795-827/Domain: ankyrin repeat
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Matches 17; Conservative
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Matches 17; Conserv
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Rilambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Ke Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A;Title: cDNA sequence for human erythrocyte ankyrin.
A;Reference number: A35049; MUID:90175370; PMID:1689849
A/Status: prei....
A/Molecule type: mRNA
A/Residues: 1-1856 <LAM>
C/Genetics: 1-1856 <LAM>
A/Cross-references: GDB:118737; OMIM:182900
A/MODE STATE AND ALCHORY CONTROLLS CONTRO
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AjGross-references: GDB:118737; ONIM:182900
Ajdene: GDB:ANK1; ANK
AjGross-references: GDB:118737; ONIM:182900
Ajdene: GDB:11-2-8D11.2
Ajdene: GDB:11-2-8D11.2
Ajdene: GDB:11-2-8D11.2
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Ajdene: GDB:11-2-8D1.2
Ajdene: GDB:11-2-8D1.2
Ajdene: GDB:11-12-12
Ajdene: GDB:11-12
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NyAlternate names: ankyrin 2.1, erythrocyte; ankyrin-R
NyContains: ankyrin 2.2, erythrocyte
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
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A;Residues: 1-1880 <LAM>
A;Cross-references: UNIPROT:P16157; GB:M28880
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Matches 14; Conservative
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R;White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.B.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992
A;Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory dom
A;Reference number: I49502; MUID:92345717; PMID:1386265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   əsidues: 1-1862 <RES>
ross-references: UNIPROT:Q02357; GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940
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C. Accession: B35049

R. Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A. Prittle: CDNA sequence for human erythrocyte ankyrin.

A. Reference number: A35049; MUID:90175370; PMID:1689849

A. Accession: B35049
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N'Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N'Contains: ankyrin 2.2, erythrocyte
C'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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Pred. No. 0.0028;
4; Mismatches 6; Indels
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                                                    Pred. No. 0.0028;
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'Molecule type: mRNA
'Residues: 1-1862 <RES>
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                                                                                                                                                                                                                  1413 DRVEMRMAVIREHLGLSWAELAREL 1437
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A;Cross-references: UNIPROT:031589; GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12720.1 A;Experimental source: strain 168
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Fi74-70 Domain: ankyrin repeat homology <ANU2>
Fi77-109/Domain: ankyrin repeat homology <ANU3>
Fi110-142/Domain: ankyrin repeat homology <ANU3>
Fi110-142/Domain: ankyrin repeat homology <ANU3>
Fi123-274/Domain: ankyrin repeat homology <ANU6>
Fi205-237/Domain: ankyrin repeat homology <ANU6>
Fi205-237/Domain: ankyrin repeat homology <ANU6>
Fi201-203/Domain: ankyrin repeat homology <ANU6>
Fi201-203/Domain: ankyrin repeat homology <ANU6>
Fi201-202/Domain: ankyrin repeat homology <ANU1>
Fi201-202/Domain: ankyrin repeat homology <ANU1>
Fi403-435/Domain: ankyrin repeat homology <ANU1>
Fi403-435/Domain: ankyrin repeat homology <ANU1>
Fi202-534/Domain: ankyrin repeat homology <ANU1>
Fi502-667/Domain: ankyrin repeat homology <ANU1>
Fi502-691/Domain: ankyrin repeat homology <ANU1>
Fi601-633/Domain: ankyrin repeat homology <ANU1>
Fi601-633/Domain: ankyrin repeat homology <ANU1>
Fi601-633/Domain: ankyrin repeat homology <ANU2>
Fi601-631/Domain: ankyrin repeat homology <ANU2>
Fi613-1382/Domain: ankyrin repeat homology <ANU2>
Fi613-1382/Bomain: Spectrin binding <ANU3>
Fi613-1382/Boma
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41.0%; Score 57; DB 2
Best Local Similarity 47.8%; Pred. No. 1.6;
Matches 11; Conservative 6; Mismatches
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F;1383-1881/Domain: 55K #status predicted <DOM3>
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nes 14; Conservative
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NyAlternate names: ankyrin 2.1, erythrocyte; ankyrin-R
NyAlternate names: ankyrin 2.1
C;Species: Hono appiens (man)
C;Becies: John, X.M.; Bennett, V.
Nature 344, 36-42, 1990
Nature 346, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42, 36-42,
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A;Map position: 8p11.2-8p11.2
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing; phosphoprotein
F;2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MATI>F;2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MATI>F;2-827/Domain: 89K #status predicted <DOMI>
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F/403-402/Domain: ankyrin repeat ho
F/403-640/Domain: ankyrin repeat ho
F/409-501/Domain: ankyrin repeat ho
F/502-534/Domain: ankyrin repeat ho
F/503-567/Domain: ankyrin repeat ho
F/561-603/Domain: ankyrin repeat ho
F/601-633/Domain: ankyrin repeat ho
F/634-666/Domain: ankyrin repeat ho
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56.0%;
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F;733-765/Domain: ankyrin repeat
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Best Local Similarity
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                                                                                                         F;337-369/Domain:
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97 EHIEERMAFLYDHILISDQEIAK 119

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probable ATP-binding protein - Streptomyces coelicolor C;Species: O: Jec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T36100 B;Saunders, D: Harris, D: Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. A;Reference number: Z21596 A;Accession: T36100 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-489 < SAUS A;Cross-references: UNIPROT: O9X873; EMBL;AL049661; PIDN: CAB41216.1; GSPDB:GN00070; SCOED A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyperiors Escherichia coli
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Cyperiors 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
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Cypate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
Rybatener, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Resion: Complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: C64935
A; Statues: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-496 < BLAT>
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A;Experimental source: strain K-12; substrain MG1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.4%; Score 52; DB 2; Length 489; Best Local Similarity 44.0%; Pred. No. 13; Matches 11; Conservative 6; Mismatches 8; Indels
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Q60202 mus musculu
Q6027 poephila gu
Q70510 rattus norv
Q9hQp5 homo sapien
Q8745 mus musculu
Q6273 homo sapien
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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ANK1 HUMAN
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ANK1 HUMAN
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Maximum Match 100%
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Q61307
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Aas52298 ashbya go P97031 bacillus su O31589 bacillus su

Q82m73 streptomyce Q8epa9 oceanobacil Q72k85 thermus the Aas80910 thermus t Q9p5x0 neurospora Q6ce33 yarrowia li Q8e4nt streptococc Q75nz5 chlamydom Bad13491 chlamydom Bad13492 chlamydom Q87ke7 vibrio para Q8sub7 encephalito Q7dym4 giardia lam Q725r8 desulfovibr	odate) prata; Euteleostomi; inidae; Homo. Amid C., Osanger A., databases.	Length 965; ; Indels 0; Gaps 0; ate) ate, ata; Euteleostomi;
40.3 384 2 Q82M73 39.6 465 2 Q8ERA9 38.8 433 2 Q72K85 38.8 433 2 Q72K85 38.8 605. 2 Q9P5X0 38.5 1201 2 Q6CE33 38.1 77 2 Q8EAN4 37.8 602 2 EAD13491 37.8 602 2 EAD13492 37.4 157 2 Q8CE7 37.4 335 2 Q72K8	RELIMINARY; PRT; 965 AA. TrEMBLrel. 25, Created) TrEMBLrel. 25, Last sequence upda protein DKFZp686M09125 (Fragment) M09125; Last annotation up protein DKFZp686M09125 (Fragment) M09125; Chordata; Craniata; Verteb trazoa; Chordata; Craniata; Verteb trazoa; Chordata; Catarrhini; Hominó, N.A. Userus; Boecher M., Mewes H.W., Weil B., M., Wiemann S.; CADS8033.1; C. CADS8035.1; C. CADS8055.1; C. CADS8055EB	Similarity 96.0%; Pred. No. 8.1e-09; 4; Conservative 0; Mismatches 1; Indels 0; 5: ERIEERLAYIADHLGFSWTELARAL 26
332 334 334 335 336 337 337 338 338 338 338 338 34 44 42 52 52 52 52 52 53 54 54 54 52 53 54 54 54 54 54 54 54 54 54 54 54 54 54	11 1 244 Q72344 Q72344; Q1-0cT-2003 Q1-0cT	Match Local S Les 24 Les 24 Local S Lo
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TISSUBE-Brain stem;
MEDLINE=91302466; PubMed=1830053;
Otto E., Kunimnoto M., McLaughlin T., Bennett V.;
"Isolation and characterization of cDNAs encoding human brain ankyrins reveal a family of alternatively spliced genes.";
J. Cell Biol. 114:221-253(1991).
P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

A Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

R Submitted (Jun.2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX537758; CAD978271; --

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR00210; AMK.

R InterPro; IPR00210; AMK.

R InterPro; IPR00196; ZUS.

R Pfam; PF00023; Ank; 23.

R Pfam; PF00023; Ank; 23.

R R Pfam; PF000248; ANK; REPEAT; 20.

R SWART; SM0005; DEATH; 1.

R RSWART; SM0005; DEATH; 1.

R PROSITE; PS5029; ANK; REP REGION; 1.

R PROSITE; PS5029; ANK REP REGION; 1.

R PROSITE; PS50017; DEATH DOWANN; 1.

ANK REPEAT; 20.

R PROSITE; PS50017; DEATH DOWANN; 1.

ANK REPEAT; 20.736 MW; IP4C99BE0F0A03DF CRC64;
                                                                                                                                                                                                                                          Gaps
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Chan W., Kordeli E., Bennett V.;
"440-kD ankyrinB: structure of the major developmentally regulated
domain and selective localization in unmyelinated axons.";
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 463-495 FROM N.A. MEDLINE-92009921; PubMed=1833308; Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E., Lux S.E., Ward D.C., Forget B.G.; "Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ankyrin gene.";
Genomics 10:858-866(1991).
-!- FUNCTION: Attach integral membrane proteins to cytoskeletal
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                         Q014E4; Q01485;
01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
O5-UUL-2004 (Rel. 44, Last annotation update)
Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid)
                                                                                                                                                                                                                      Length 1863;
                                                                                                                                                                                                                     88.5%; Score 123; DB 2; Length 18
96.0%; Pred. No. 1.6e-08;
ive 0; Mismatches 1; Indels
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Brain stem;
                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Best Local Similarity 96.0'
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Ankyrin 2, brain.
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in isoform 2).
FTId=VSP_000267.
                                                                                                                                                                                                                                                                                                                                      Missing (In isoform 2 and isoform 3).
/FIId=VSP 000268.
GQ -> PE (In Ref. 4).
I -> S (in Ref. 1).
I -> Y (in Ref. 1).
I -> Y (in Ref. 1).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 3.3e-08;
0; Mismatches 1; Indels (
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Best Local Similarity 92.0%; Pred. No. 2.4e-08;
Matches 23; Conservative 1; Mismatches 1; Indels
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Strausberg R.;
Strausberg R.;
Submitteed (JAN-2203) to the EMBL/GenBank/DDBJ databases.
EMBL; BC043123; AAH43123.1;
GO; GO:0007155; P:signal transduction; IEA.
InterPro; IRR001029; Death.
InterPro; IRR011029; DEATH_like.
Fram; PRO051; Death; 1.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1038 AA; 114518 MW; 3012ED0E9AA2A0F4 CRC64;
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01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to ankyrin 2, neuronal (Fragment).
                                                                                                                                        (approximate)
                                                                                                                                                                                        (approximate)
 Repeat-rich region.
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                    Repeat A.
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 88.5%;
Local Similarity 96.0%;
es 24; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 430337
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3582
3586
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3581 358
3586 358
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                1903
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CONFLICT
CONFLICT
SEQUENCE
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VARSPLIC
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Matches
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0280227
1D 080220
DT 01-J
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
enriched library, clone:6330566N20 product:ankyrin 2, neuronal long
Name=Ank2;
                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Straushery R.;
Submitted (CCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO5921, AAH59251.1;
InterPro; IPR001029; DEATH like.
InterPro; IPR001029; DEATH like.
InterPro; IPR001029; DEATH, 1.
Ffam; PF00531; Death; 1.
SYART; SM00005; DEATH; 1.
SYART; SM02005; DEATH; 1.
SYART; SM02018; ZUS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match B6.3%; Score 120; DB 2; Length 1050; Local Similarity 92.0%; Pred. No. 2.4e-08; es 23; Conservative 1; Mismatches 1; Indels
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                                 Created)
Last sequence update)
Last annotation update)
PRT; 1050 AA.
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
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PRELIMINARY;
                Q6PCN2;
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                       Mus musculus (Mouse).
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Q8CCV0
ID Q8CC
D7 01-M
DT 01-M
DD MUS
DE SPILI
GN NAME
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AAH59251
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Q9DEY7;
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Q9DEY7
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashlaume M.,
Rukuda S., Furuno M., Hanagaki T., Hara A., Hashlaume M.,
Hayashida K., Hayatsu M., Hiramoco K., Hiraoka T., Hirozane T.,
Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Munata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe V., Tagami M.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Jomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (UJUL-201) to the EMBL/GenBank/DDBJ databases.

R GD; MGI:88025; Ank2.

R GD; MGI:88025; Ank2.

R GJ; GG:0001155; Psignal transduction; IEA.
                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDMAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; IISSUB=Medulla oblongata; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CS7BL/GI, TISSUE=Medulla oblongata;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Suminoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kabilwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Matahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Nazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                           STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=9927953; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE-Medulla oblongata;
The FANTOM Consortium,
                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUB=Medulla oblongata;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
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InterPro; IPR011029; DEATH_11ke.
InterPro; IPR000906; ZUS.
Pfam; PF00531; Death; 1.
Pfam; PF00791; ZUS; 1.
SWART; SM00005; DEATH; 1.
Mus musculus (Mouse)
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain;

RUDINE=2528825; PubMed=1247932;

SA Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N. K.,

Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N. K.,

Altschul S.F., Zeeberg B. Buecow K.S. I., Wang J., Hebich F.,

Antichal R.P., Jordan H., Moore T., Max S. I., Mand J., Hong L.,

Antichal R. S., Jordan H., Moore T., Max S. I., Mand J., Hong L.,

Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Morley K.C., Hale S., Garcia A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A., Gubbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A., Gubbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Hitchyles R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                 Length 1050;
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92.0%; Pred. No. 2.4e-08;
iive 1; Mismatches 1; Indels
SMART; SM00218; ZUS; 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
SEQUENCE 1050 AA; 117402 MW; E9E52A618E06DBA6 CRC64;
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCG5921; AAH5925.1; -.
SEQUENCE 1050 AA; 117435 MW; BODD8C0591A8F177 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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                                                                                                                    86.3%; Score 120; DB 2; 92.0%; Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1050 AA.
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                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                    611 ERMEERLAYIADHLGFSWTELAREL 635
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STRAIN=C57BL/6; TISSUE=Brain;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 92.0°
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
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Created)
Last sequence update)
Last annotation update)

PRT;

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TISSUB-Kidney;
Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
L. Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
R. BMBL; AL186710; CABG6645.1; -.
R. BMBL; AL186710; CABG6645.1; -.
R. GO; GO:0007165; P:signal transduction; IEA.
R. InterPro; IPR000489; Death.
R. InterPro; IPR000906; ZUS.
R. Finerpro; IPR000906; ZUS.
R. Ffam; PP00531; Death; 1.
R. FMART; SM00018; ZUS; 1.
R. SMART; SM0018; ZUS; 1.
R. SMART; SM00218; ZUS; 1.
R. RAART; SM00218; ZUS; 1.
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 64.7%; Score 90; DB 2; Length 811; Local Similarity 68.0%; Pred. No. 0.0004; les 17; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. - SEQUENCE 811 AA; 90104 MW; F180C76C34AB1D4A CRC64;
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                        Q9HOP5;
01-MAR-2001 (TrEMBLrel. 16, Last se
01-MAR-2001 (TrEMBLrel. 16, Last se
01-MAR-2004 (TrEMBLrel. 26, Last an
Hypothetical protein DKPZp566P0524.
Name=DKFZp566P0524;
  PRELIMINARY;
                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               IISSUE=Kidney
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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K MEDLINE=98330444; PubMed=9664041;

A Kordell E., Ludosky M.A., Deprette C., Frappier T., Cartaud J.;

A Kordell E., Ludosky M.A., Deprette C., Frappier T., Cartaud J.;

Kordell E., Ludosky M.A., Deprette C., Frappier T., Cartaud J.;

I Sarcoplasmic reticulum in the skeletal muscle fiber.";

J. Cell Sci. 111:12197-2207(1998).

E MEL, AF065149; AAC18852.1;

R GO, GO:0007165; P:signal transduction; IEA.

R InterPro; IPR0100489; Death.

R InterPro; IPR010029; DEATH.like.

R Pfam; PF00531; Death; 1.

R RROSITE; SM00005; DEATH; 1.
                  Poephila guttata (Zebra finch) (Taeniopygia guttata).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taehiopygia.
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68.0%; Pred; No. 6.9e-05; Indels
                                                                                                                                                                SEQUENCE FROM N.A.
SOGERSTROM K., JOHNSON F.;
SOGERSTROM K., JOHNSON F.;
SUDMITTEG (SEP-2000) to 7.16
EMBL; AR307862; AAG29827.1; -.
GO; GO:0007165; P:signal transduction; IEA.
INCERPO; IPR0010488; Death.
InterPro; IPR011029; DEATH_like.
Pfam; PR00531; Death; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23245 MW; 6A8745802F496877 CRC64;
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Last annotation update)
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Ankyrin B (Fragment)
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Best Local Similarity
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070510
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Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Skin;
MEDLLINE=21103470; Pubmed=11179996;
Peters B., Kaiser Hw., Magin T.M.;
"Skin-specific expression of ank-3(93), a novel ankyrin-3 splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.7%; Score 90; DB 2; Length 838;
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                                                                                                                                                                                                                                                                                                                                                 __MAY_2000 (TrEWBLrel. 13, Created)
|-MAY-2000 (TrEMBLrel. 13, Last sequence update)
|-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U. M. West. Dermatcl. 116:216-223 (2001).

EMBL, AF212924; AAF18477.1; ---
EMBL, AF212924; AAF18477.1; ---
GO, GO:0042202; ARS. MAS. GO, GO:0042202; C: Synapse; IDA.

InterPro; IPRO00488; Death.

InterPro; IPRO00488; Death.

InterPro; IPRO00906; ZUS.

Pfam; PF00791; ZUS.

Pfam; PF00791; ZUS.

SWART; SM00005; DEATH; 1.

SWART; SM0218; ZUS; 1.

SRART; SM0218; ZUS; 1.

SEQUENCE 838 AA; 93352 MW; 67319A932E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ankyrin-3 skin-specific splice variant
609 ERTDIRMAIVADHLGLSWTELAREL 633
                                                                                                                                                                                                                                                                  PRT;
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RESULT 10

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609 ERTDIRMAIVADHLGLSWTELAREL 633
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X MEDLINE=2193531; PubMed=11796721;

Gagelin C. Constantin B., Deprette C., Ludosky M.A., Recouvreur M.,

Cartand J., Cognard C., Raynond G., Kordeli E.;

T. Gattification of AnkGl07, a muscle-specific ankyrin-G isoform.";

J. Biol. Chem. 277:129378-12987 (2002).

REMBL, AJ428573; CAD21705.1;

RO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR0101029; DEATH.

R InterPro; IPR0101029; DEATH.

R Pfam; PF00331; Death.

R Pfam; PF00331; Death.

R Pfam; PF0031; Ju Death.

R SMART; SM00105; DEATH; 1.

R SMART; SM00105; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male urinary bladder cDNA, RIKEN full-length
enriched library, clone:9530086C08 product:ankyrin 3, epithelial, full
                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
            Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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68.0%; Pred. No. 0.00047;
iive 3; Mismatches 5; Indels
 68.0%; Pred. No. 0.00041;
tive 3; Mismatches 5; Indels
                                                                                                                              Created)
Last sequence update)
Last annotation update)
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                                                                                                            960 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1093 AA.
                                            596 ERTDIRMAIVADHLGLSWTELAREL 620
                                 2 ERIEERLAYIADHLGFSWTELARAL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ERIEERLAYIADHLGFSWTELARAL 26
                                                                                                           PRT;
                                                                                                                              01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
Ankyrin G107.
Best Local Similarity 68.0%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                           PRELIMINARY;
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C STRAIN=CS7BL/G0; TISSUE=Urinary bladder;
A dachi U. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A Fukuda S., Furuno M., Haragaki T., Hasa A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai U., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takakashi F., Takaku-Akahira S., Takaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRANIE-STBL/GAJ TISSUE=Urinary bladder;
The FANTOM CONSORTIUM.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CS7BL/G0; TISSUB=Urinary bladder;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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STRAIN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CSTBALN=CST
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                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Pred. No. 0.00053;
3; Mismatches 5; Indels
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SMART; SM00005; DEATH; 1.
SMART; SM0018; ZU5;
PROSITE; PS50017; DEATH DOMAIN; 1.
SEQUENCE 1093 AA; 121089 MW; 4AA982E4FB1D9CF5 CRC64;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Urinary bladder;
STRAIN=E2108566J; PubMed=11217851;
RIKEN FANTOM CORSOTTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ERIEERLAYIADHLGFSWTELARAL 26
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InterPro; IPRO10488; Death.
InterPro; IPRO11029; DEATH_like.
InterPro; IPRO10906; ZUS.
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Pfam; PF00791; ZU5; 1.
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Best Local Similarity
Matches 17; Conserv
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Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Wurakawa K., Kanehori K., Masuho Y., Nagai K., Isogai T.;
WnEDO human CDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AK12681; BAG8721.1;
SEQUENCE 1101 AA; 122188 MW; 321372D4C0A60856 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Amygdala;
OSSIMEA A. Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irise R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Satoo K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Nakamura Y., Sugiyama A., Kawakami B., Suuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK126851; BAC86721.1.
Embl. AK126851; BAC86721.1.
EnterPro; IPR000488; Death.
InterPro; IPR000906; ZUS.
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BAC86721,
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
HOMO sapiens (Human).
ENCARYON (Human).
ENCARYON (Human).
ENCARYON (MERAZOA; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FL744903.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00531; Death; 1.
Pfam; PF00791; 2U5; 1.
SNART; SM00005; DeaTH; 1.
SNART; SM0018; ZU5; 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
SRQUENCE 1101 AA; 122188 MW; 321372D4C0A60856 CRC64;
                                                                                                                  PRT; 1101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                710 ERTDIRMAIVADHLGLSWTELAREL 734
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                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                             Q6ZT73
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BAC86721
DD CACMA
DT 02-MA
RA OSHI
RA OSHI
RA AKI
R
RESULT 14
062273
AC 06227
DT 05-JU
DT 0
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64.7%; Score 90; DB 2; Length 1101;

Search completed: November 10, 2004, 12:27:26 Job time : 30.4475 secs This Page Blank (uspto)

us-10-092-750-224.rai

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November 10, 2004, 14:55:47; Search time 5.08897 Seconds (without alignments) 143.349 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                 Run on:
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BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-092-750-224 63 1 KYQQLFEDIRW 11 Title: Perfect score: Scoring table: Sequence:

478139 seqs, 66318000 residues Searched:

478139

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1		ر مو				
i	Score	Match	Length	DB	ID	Description
	42	66.		4	-13	Sequence 3595, Ap
	40		ø	4	4-272A	equence 3,
	39		9	4	-65	e 10,
	39	61.9	374	ო	-09-045-583-	equence 4
	39		7	4	34-18	equence 48,
	39		4	m	-09-291-922-30	equence 30,
	38		m	4	-09-134-000C-40	equence 403
	38		3	4	-09-583-110-2	equence 295
	38		4	ო	-08-960-180-	e 25,
	38		4	ო	-09-073-898-2	equence 25,
	38		4	4	-00-307-106-	equence 6,
	38		4	4	-09-850-351A-	equence 25,
	38		4	ო	-08-960-780-2	equence 21,
	38		4	ო	-08-960-780-	equence 42,
	38		4	m	-09-073-898-2	equence 21,
	38		4	m	-09-073-898-4	equence 42,
	38		4	4	۳	equence 21,
	38	60.3	348	4	-038-60-	equence 42
	38		g	Н	-08-138-641-	equence 2,
	38		29	H	-08-138-13	4
	38		29	4	US-09-538-092-956	926
	37		4	m	-89	14
	37		4	4,	US-09-307:106-34	34, A
	37	٠.	4	4	-09-850-351A-1	equence 14
	36	57.1	54	4	-09-270-767-	37516
	36		54	4	US-09-270-767-52733	equence 52733
	36		207	4	US-09-489-039A-13743	Sequence 13743, A

38, 9, p	Sequence 11, Appl Sequence 11, Appl Sequence 3, Appli Sequence 2, Appli	444	446	Sequence 2, Appil Sequence 120, App Sequence 75, Appil Sequence 75, Appil	1961
US-08-602-359A-38 US-09-355-166-4 US-09-462-845-9	US-09-910-174B-11 US-09-620-461-11 US-08-424-788-3 US-08-424-788-2	US-08-110-683-4 US-08-477-166-4 US-08-472-097-4	US-09-439-672-4 PCT-US93-11638-4 US-08-724-394A-3	US-10-305-640-2 US-10-140-002-120 US-08-683-262B-75 US-09-361-707-75	US-09-252-991A-19615
01 W 44	4444	400	4000	u 4.01 W	4
300 305 305	523 523 523 523 523	575 575 575	575 575 581	973	142
57.1 57.1 57.1	57.1 57.1 57.1	57.1 57.1 57.1	57.1	57.1	22.6
36 36	9 9 9 9 9 9 9 9	999	9999	9 9 9 9 9 9 9 9	32
309 309	333 333 34 34	3 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	338 8664 8664	4 4 4 4 1 2 6 4	45

ALIGNMENTS

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Sequence 3955, Application US/09134000C
| Patent No. 6617156
| GENERAL INFORMATION: 6617156
| GENERAL INFORMATION: WUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: WUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: WURRECCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032 | CURRENT FILING DATE: 1990-08-13 | FILE REFERENCE: 032796-012 | FILE REPRINCE: 032796-012 | FILE REPRINCE: 032796-013 | FILE REPRINCE: 032796-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KYQQLFEDIR 10
|:||||||
131 KFQALFEDIR 140
US-09-134-000C-3595
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RESULT 2
US-09-914-272A-3
Sequence 3, Application US/09914272A
Sequence 3, Application US/09914272A
Sequence 3, Application US/09914272A
Sequence 3, Application US/09914272A
SEPERAL INFORMATION:
APPLICANT: Sakaguchi, No. 6673913uo
APPLICANT: Sakaguchi, No. 6673913uo
APPLICANT: Ruwahaza, Kazuhiko
TITLE OF INFORMION: GANP Protein
FILE OF INNUMIEN: 050208-0014
CURRENT APPLICATION NUMBER: US/09/914,272A
CURRENT FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
TYPE: PRI

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FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MANDIAGOURAER: 36,207
REFERENCE/DOCKEY NUMBER: 36,207
REFERENCE/DOCKEY NUMBER: MAI-
TELECHONE: (617)227-7400
TELECHONE: (617)227-7400
TELECHONE: (617)227-7401
TELECHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: USA
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.6.
Since 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-48
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GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled CORRESPONDENCE. 56
CORRESPONDENCES: 56
CORRESPONDENCES: ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STRIE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Wei,
APPLICANT: Wang, Wei,
APPLICANT: Gish, Kurt C.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Thomas J.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Antibodies that bind chemokine TECK
TITLE OF INVENTION: DAGSSAKE US
CURRENT FILING DATE: 1090-01-03
CURRENT FILING DATE: 1997-07-03
PRIOR APPLICATION NUMBER: US 60/021,664
PRIOR FILING DATE: 1996-07-05
STOR FILING DATE: 1996-07-05
STOR FILING DATE: 1996-07-05
STOR FILING DATE: 1996-07-05
STOR FILING DATE: 1997-06-04
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 10
LENGTH: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/10039659A Patent No. 6723520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09045583
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                                                                                                                                         Query Match 63.5%;
Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                          1329. YQQLLSDVAW 1338
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ORGANISM: Homo sapiens
                                  ; ORGANISM: Homo sapiens
US-09-914-272A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-10-039-659A-10
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Sequence 48, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 640376761 Molecules of the G Protein-Coupled
TITLE OF INVENTION: Heptahelical Receptor Superfamily and Uses
Score 39; DB 3; Length 374;
Pred. No. 61;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: MANDERS, AMY E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                        Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 374 amino acids
TYPE: amino acid
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| Patent No. 6617156
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al FITILE OF INVENTION: ENFENCECCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFRENCE: 032796-032
| CURRENT APPLICATION NUMBER: US 60/055,778 | PRIOR FILING DATE: 1997-08-15 | NUMBER OF SEQ ID NOS: 6812 | NUMBER OF SEQ ID NOS: 6812 | SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                             Gaps
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                                                                            Score 39; DB 4; Length 374;
Pred. No. 61;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 3; Length 549;
Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                    RESULT 6
US-09-291-922-30
| Sequence 30, Application US/09291922
| Sequence 30, Application US/09291922
| Sequence 30, Application US/09291922
| GENERAL INFORMATION:
| APPLICANT: Allen, Steve |
| APPLICANT: Hincy, Hill |
| APPLICANT: Tingey, Scott |
| TILE OF INVENTION: Plant Sugar Transport Proteins |
| FILE REPERSNCE: BB-1163 |
| CURRENT APPLICATION NUMBER: US/09/291,922 |
| CURRENT PILING DATE: 1999-04-14 |
| EARLIER APPLICATION NUMBER: 60/083,044 |
| EARLIER FILING DATE: April 24, 1998 |
| WUMBER OF SEQ ID NOS: 30 |
| SEQ ID NO 30 |
| LENGTH: 549 |
| TYPE: PRT |
| ORGANISM: Beta vulgaris |
| US-09-291-922-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-534-185-48
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US-09-134-000C-4038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.9%;
75.0%;
                                                                               Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conservative
                                                                                                                                                                                                 200 KYQTVSEPIRW 210
                                                                                                                                                                   1 KYQQLFEDIRW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                498 ELFEDFRW 505
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43 QFQQLFEDV 51
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US-09-134-000C-4038
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LENGTH: 232
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yearunce_2957, Application US/09583110
| Sequence_2957, Application US/09583110
| Patent No. 6699703
| GENERAL INFORMATION:
| APPLICANTY Lynn Doucette-Stamm et al.
| TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus;
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus;
| TITLE OF INVENTION: NurMERR: US (09/107,433)
| PRIOR FILING DATE: 1998-06-10
| PRIOR PLING DATE: 1998-06-10
| PRIOR PLING DATE: 1998-05-12
| PRIOR PLING DATE: 1998-05-12
| PRIOR PLING DATE: 1998-05-12
| NUMBER OF SEQ ID NOS: 5322
| LEGITH: 236
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; Sequence 25, Application US/08960780
; Patent No. 6204435
; GENERAL INFORMATION
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Stockhoff, Brian A.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Lower, James
; APPLICANT: Lower, David
; APPLICANT: David
; APPLICANT: Muller-Cohn, Judy
; APPLICANT: Stamp, Lisa
; TITLE OF INVENTION: Sequences Which Encode These Toxins
number of SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; STREET: C. Saliwanchite C. STREET: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 58;
2; Mismatches 1; Indels
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; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.3%;
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Best Local Similarity 70.0
Matches 7; Conservative
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TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
    SEQUENCE CHARACTERISTICS
                                                                                TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-307-106-6
                                            LENGTH:
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APPLICANT: Schnepf, H. Brnest
APPLICANT: Schnepf, H. Brnest
APPLICANT: Schneits, James
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Loewer, David
APPLICANT: Muller-Cohn, Judy
APPLICANT: Morrill, George
APPLICANT: Morrill, George
APPLICANT: Morrill, George
APPLICANT: Stance, Staccey
TITLE OF INVENTION: Sequences Which Encode These Toxins
ANDMERS OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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Pred. No. 84;
2; Mismatches 3; Indels
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ZIP: 32606-6669
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-OCT-1996
FILING DATE: 30-OCT-1996
PRIOR APPLICATION NUMBER: US 08/960, 780
FILING DATE: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09073898
Patent No. 6242669
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-775-8100
TELEPHONE: 352-372-800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KYQQLFEDIRW 11
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US-09-073-898-25
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APPLICANT: Stamp. Judy
APPLICANT: Morrill, George
APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 6603663el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchit.
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                               Score 38; DB 3; Length 347; Pred. No. 84; 3; Indels 2; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US/09/307,106
FILNG APPLICATION NUMBER: US 60/029,848
FILNG APPLICATION NUMBER: US 60/029,848
FILNG APPLICATION NUMBER: US 60/029,848
FILNG APPLICATION NUMBER: US 80/960,780
FILNG APPLICATION NUMBER: US 08/960,780
FILNG APPLICATION NUMBER: US 09/073,898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....ode T. ...wkESS:
...wkESS:
STREE: Saliwanchik, Lloyd & Saliwanchik
STREE: 2421 N.W. 41st Street, Suite A-1
CITY: Gainsville
STATE: FL
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE FOCKET NUMBER: MA-708C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feitelson, Jerald S. Schnepf, H. Ernest Narva, Kenneth E. Stockhoff, Brian A. Schmeits, James Loewer, David Dullum, Charles Joseph Miller-Cohn, Judy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09307106
Patent No. 6603063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE: INDIVIDUAL ISOLATE: 66D3 US-09-073-898-25
: 347 amino acids
amino acid
                                                 single
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                                                                4; Length 347;
                                                                                         3; Indels
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Pred. No. 84;
2; Mismatches
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; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-850-351A-25
                                                                 Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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INDIVIDUAL ISOLATE: 31J2
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38 KQQQTYQSIRW 48
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                                                                                                                    1 KYQQLFEDIRW 11
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                                                                                                                                                                                                                                                                                                   APPLICANT: Feitelson, Jerald S.
Schnepf, H. Ernest
Narva, Kennerh E.
Stockhoff, Barian A.
Schweits, James
Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
Morrill, George
TITLE OF INVENTION: No. 6656908el Pesticidal Toxins and Nucleotide
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CONDUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

CONFUTER: IBM PC compatible

CONFUTER: BENEVALION

CONFORTING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

PRIOR APPLICATION NUMBER: US 09/073,898

FILING DATE: 06-M8Y-1998

FILING DATE: 06-M8Y-1998

FILING DATE: 06-M8Y-1998

FILING DATE: 06-M8Y-1998

FILING DATE: 30-CCT-1997

APPLICATION NUMBER: US 08/960,780

FILING DATE: 30-CCT-1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                  60.3%; Score 38; DB 4; Length 347; 54.5%; Pred. No. 84; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2441 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sanders, Jay M. REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708CD1
TELECOMMUNICATION:
                                                                                                                                                                                                                                    RESULT 12
US-09-850-351A-25
Sequence 25, Application US/09850351A
Patent No. 6656908
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 352-375-8100
TELEPAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 347 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
CORLIGULE TYPE: peptide
CORLINAL SOURCE:
INDIVIDUAL ISOLATE: 66D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                Best Local Similarity 54.9
Matches 6; Conservative
                                                                                                                                                                                     38 KQQQTYQSIRW 48
                                                                                                                                                                      1 KYQQLFEDIRW 11
                                                                                                                     Query Match
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Gaps

39 KOQQTYQSIRW 49

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APPLICANT: Feitelson, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schneit E.
APPLICANT: Schneits, James
APPLICANT: Loewer, David
APPLICANT: Loewer, David
APPLICANT: Loewer, David
APPLICANT: Stamp, Lisa
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sallwanchik, Licyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
GITTE Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.3%; Score 38; DB 3; Length 348; Best Local Similarity 54.5%; Pred. No. 84; Matches 6; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US

SIGNED 32606-6669

COMPUTER READBLE PORN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
FLING DATE: 30-OCT 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT 1996
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REGISTRATION FOR SEQ ID NO: 42:
SEQUIRONE SEQ ID NO: 42:
SEQUIRONE CHARACTERISTICS:
US-08-960-780-42
Sequence 42, Application US/08960780
Patent No. 6204435
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/09073898; Patent No. 624269; GENERAL INFORMATION: APPLICANT: Feitelson, Jerald S. APPLICANT: Schnepf, H. Ernest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; INDIVIDUAL ISOLATE: 197T1
US-08-960-780-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 KQQQTYQSIRW 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KYQQLFEDIRW 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-073-898-21
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APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James
APPLICANT: Schmeits, James
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Deaver, David
APPLICANT: Muller-Cohn, Judy
APPLICANT: Muller-Cohn, Judy
APPLICANT: Morrill, George
APPLICANT: Stance-Leo, Stancey
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPENDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STAREF: 2421N.W. 41st Street, Suite A-1
CITY: Galnesville
STATE: Leomographic Compatible
COUNTRY: US
ZIP: 3266-6669
ZIP: 3266-669
ZOMPUTER: READABLE FORM:
MEDIUM TYPE: Potentin Release #1:0, Version #1:30
CURRENT APPLICATION NUMBER: US/09/073,898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 10, 2004, 15:57:23 Job time : 6.08897 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C1
TELESPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: 31J2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KYQQLFEDIRW 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-073-898-21
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Query Match
Best Local S:
Matches 11
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 224, App
Sequence 3906, Ap
Sequence 74458, A
                                                                                                                      November 11, 2004, 02:43:24; Search time 26.5801 Seconds (without alignments) 146.426 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3900
Sequence 7445
Sequence 45,
Sequence 10,
Sequence 10,
Sequence 10,
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Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA:*

l: /cgn2_6/ptodata/2/pubpaa/Pcr_NEW PUBCCMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/Pcr_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/Pcr_NEW PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USIOP_PUBCCMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-092-750-224
US-10-369-493-3906
US-10-282-1224-74458
US-10-239-423-44
US-10-239-423-44
US-10-239-423-49
US-10-754-071-10
US-10-754-071-10
US-10-239-423-69
US-10-164-649-48
US-10-164-649-48
US-10-087-423-68
US-10-087-423-68
US-10-087-423-68
                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                       1568699 segs, 353819137 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                          US-10-092-750-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                           1 KYQQLFEDIRW 11
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Match Length
                  Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                           Run on:
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Sequence 40, Appl
Sequence 30, Appl
Sequence 345726,
Sequence 345726,
Sequence 13450, A
Sequence 74155, A
Sequence 74155, A
Sequence 17035,
Sequence 17035,
Sequence 31072, A
Sequence 17035,
Sequence 17035,
Sequence 17035,
Sequence 2728, A
Sequence 30757,
Sequence 36718, A
Sequence 5718, A
Sequence 67718, A
Sequence 6718, A
Sequence 6718, A
Sequence 6718, A
Sequence 140, Appl
Sequence 160, Appl
Sequence 170, Appl
Sequence 170, Appl
Sequence 160, Appl
Sequence 170, Appl
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Publication No. US20030032157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Julia

APPLICANT: PRIGHC, Martin C.

FILE OF INVENTION: POLYPEPTION C.

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US 60/274,526

PRIOR PELING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 224

LENGTH: 11
14 US-10-029-386-32911
10 US-09-174-381-40
11 US-09-151-902-30
12 US-10-051-909-30
13 US-10-051-909-30
14 US-10-282-123A-74155
14 US-10-282-123A-74155
15 US-09-850-351A-21
16 US-10-452-002A-6
17 US-09-850-351A-21
18 US-10-452-002A-6
19 US-09-850-351A-21
19 US-09-850-351A-21
19 US-10-452-002A-6
19 US-09-850-351A-21
19 US-10-487-963-177035
14 US-10-437-963-177035
15 US-10-425-115-36757
15 US-10-426-115-36757
15 US-10-426-115-36757
15 US-10-426-128-223
15 US-10-108-260A-4160
15 US-09-950-351A-140
16 US-09-950-351A-140
                                                                                                                                                                                                                                                                                                US-10-452-002A-34
US-10-422-599-176275
US-10-389-64-688
US-10-195-142-14
US-10-381-530-18
US-10-437-963-181535
US-10-437-963-181535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 63; DB 14;
llarity 100.0%; Pred. No. 0.00033;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3906, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYQQLFEDIRW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KYQQLFEDIRW 11
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11; Conserv
   RESULT 2
US-10-369-493-3906
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Gaps

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Publication No. US20030186889A1

Publication No. US2003018688A1

Sequence 44, Application US/10239423

Publication No. US2003018688A1

GENERAL INFORMATION:
APPLICANT: FORSEMANN, Wolf-Georg; FORSEMANN, Ulf; ADERWANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj

TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the

TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and

TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction

FILE REFERENCE: 022217us

CURRENT APPLICATION NUMBER: US/10/239,423

CURRENT APPLICATION NUMBER: DE10016013.1

PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45, Application US/10239423
Publication No. US2003018689A1
GENERAL INFORMATION,
GENERAL INFORMATION,
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proceement of Tunor and Inflammation Cells and
TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239,423
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: DE10016013.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies US-10-239-423-45
                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 74458
LENGTH: 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 15; Length 1086; Pred. No. 3.2e+02; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 14; Length 15;
Pred. No. 6.9;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Streptococcus pyogenes US-10-282-122A-74458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 84
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goddman, Barry S.
APPLICANT: Goddman, Barry S.
APPLICANT: Goddman, Palwiry M.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3906
LENGTH: 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 56;
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NAME/KEY: unsure
LOCATION: (1)..(417)
CTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 74458, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR PILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Observent Carrier
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 ORLFDDLRW 111
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Gaps

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Gequence 69, Application US/10239423

Sequence 69, Application US/10239423

Sequence 69, Application US/10239423

Sequence 69, Application No. US2030186889A1

FURDIcation No. US2030186889A1

APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;

APPLICANT: HEITLAND, Aleksandra; SPOBSBERG, Nikolaj

TITLE OF INVENTION: Delagnostic Agent and Medicament for Examining the

TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and

TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,

TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction

FILE REFERENCE: 022217us

CURRENT FILING DATE: 2002-09-23

PRIOR APPLICATION NUMBER: US/10/239,423

PRIOR APPLICATION NUMBER: D1016013.1

PRIOR PRINCE DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 365;
                                                                                                                                                                                                                                                                        APPLICANT: Wang, Wei
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Thomas J.
APPLICANT: Jourik, Albert
TITLE OF INVENTION: Chemckine TECK Polypeptides
FILE REFRENCE: DXOSSSHIC US
CURRENT APPLICATION NUMBER: US/10/754,071
FRICR APPLICATION NUMBER: US 10/039,659
PRIOR APPLICATION NUMBER: US 08/887,977
PRIOR APPLICATION NUMBER: US 08/887,977
PRIOR PRILING DATE: 1996-07-05
PRIOR PILING DATE: 1996-07-05
PRIOR APPLICATION NUMBER: US 60/021,664
PRIOR FILING DATE: 1996-10-11
PRIOR PRILING DATE: 1996-10-11
PRIOR APPLICATION NUMBER: US 60/048,593
PRIOR FILING DATE: 1996-10-11
PRIOR PRICN PRILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PALENT VERSION 3.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 16;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                       Sequence 10, Application US/10754071 Publication No. US20040137578A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 69
LENGTH: 369
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191 KYQTVSEPIRW 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Homo sapiens
US-10-754-071-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 365
TYPE: PRT
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                                                                                                                         FEATURE:
COTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-44
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CORFWARE: PatentIn Release #1.0, Version #1.30

CURRINT APPLICATION DATA:

APPLICATION NUMBER: US/10/039,659

FILING DATE: 03-Jan-2002

CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                        Score 39; DB 14; Length 30;
Pred. No. 14;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 14; Length 36
Pred. No. 1.6e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gish, Kurt C.
Schall, Thomas J.
Vicarl, Alain P.
Zlotnik, Albert
TITLE OF INVENTION: WAMMALIAN CHEMOKINE REAGENTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-JUL-1997
APPLICATION NUMBER: US 60/021,644
FILING DATE: 05-JUL-1996
APPLICATION NUMBER: US 60/028,329
FILING DATE: 11-OCT-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/887,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXG589K1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/10039659
Publication No. US20030018167A1
GENERAL INFORMATION:
APPLICANT: Wang, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 365 amino acids TYPE: amino acid
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61.9%; Soc
Best Local Similarity 63.6%; Pre
Matches 7; Conservative 1;
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                                                                                                                                                                                                                                                        61.9%;
                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44
LENGTH: 30
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                            1 KYQQLFEDIRW 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-039-659-10
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Gaps

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Sequence 68, Application US/10239423

Fublication No. US200301868931

GENERAL INFORMATION:

APPLICANT: FORSEMANN, Wolf-Georg; FORSEMANN, Ulf; ADERWANN, Knut,

APPLICANT: FORSEMANN, Wolf-Georg; FORSEMANN, Ulf; ADERWANN, Knut,

APPLICANT: HEITLAND, Aleksandra, SPODSBERG, Nikola;

APPLICANT: HEITLAND, Aleksandra, SPODSBERG, Nikola;

TITLE OF INVENTION: Call Surface Proteome of Tumor and Inflammation Cells and

TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

TITLE OF INVENTION NUMBER: US/10/239, 423

CURRENT APPLICATION NUMBER: DE10016013.1

PRIOR APPLICATION NUMBER: DE10016013.1

PRIOR PLING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 84

SEQ ID NO 68

LENGTHREE PATENTION NUMBER: DE10016013.1

SEQ ID NO 68

LENGTHREE PATENTION NUMBER: DE10016013.1

SEQ ID NO 68

LENGTHREE PATENTION NUMBER: DE10016013.1
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                  Length 374;
                                                                                                                                                                                                                                                                                                                                               Score 39; DB 14; Length 37
Pred. No. 1.7e+02;
1; Mismatches 3; Indels
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Publication No. US20020182586A1
Fublication No. US20020182586A1
FUBLICANT: MORNATION
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: OANCER
FILE REFERENCE: 529452000122
CURRENT FILLIC DATE: 2002-03-01
FRIOR APPLICATION NUMBER: US 09/747,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

61.9%; Score 39; DB 14;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 3
               TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7410
TELEPHONE: (617)227-7410
TELEPHONE: (617)227-7410
TELEPHONE: (617)227-7410
TELEPHONE: (617)227-7410
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-164-649-48
REFERENCE/DOCKET NUMBER: MNI-044
                                                                                                                                                                                                                                                                                                                                                     61.9%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.0%
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 KYQTVSEPIRW 210
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US-10-087-192-1920
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                                                                                                                                                                                                                                                                                                               Sequence 399, Application US/10225567A

Publication No. US2030113798A1

GENERAL INFORMATION

APPLICANT: LifeSpan Biosciences

APPLICANT: Burner, Glenna C.

APPLICANT: Burner, Glenna C.

APPLICANT: Burner, Glenna C.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT APPLICATION NUMBER: 60/257,144

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTHARE: PatentIn version 3.1

LENGTH: 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 48, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: No. US20030162943A1e1 Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; STREET: 28 State Street
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                                                  Length 369;
                                                  Score 39; DB 14; Length 36
Pred. No. 1.7e+02;
1; Mismatches 3; Indels
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COMPUTER READABLE FORM:

BUTDUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: S/10/164,649

FILING DATE: 07-UN-2002

CLASSIPICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-WAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.9%;
                                                       61.9%;
63.6%;
                                                     Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                          195 KYQTVSEPIRW 205
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                                                                                                                                                       1 KYQQLFEDIRW 11
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US-10-225-567A-390
                                                                                                                                                                                                                                                                                     RESULT 9
US-10-225-567A-390
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US-10-164-649-48
       US-10-239-423-69
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GENERAL INCORANTION:

APPLICANT: Holtzman, Douglas A.

APPLICANT: McCarthy, Sean A.

APPLICANT: Gearing, David P.

TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-1 MOLECULES

TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-1 MOLECULES

TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-1 MOLECULES

TITLE OF INVENTION: NOVEL EDIRF, MS/09/774,381

CURRENT APPLICATION NUMBER: 09/010,674

FRIOR FILING DATE: 1999-09-30

FRIOR FILING DATE: 1999-01-20

FRIOR FILING DATE: 1999-01-20

FRIOR FILING DATE: 1999-01-20

FRIOR PRIOR PAPLICATION NUMBER: 09/014,347

FRIOR FILING DATE: 1999-10-06

FRIOR PAPLICATION NUMBER: 09/004,206

FRIOR APPLICATION NUMBER: 09/004,206

FRIOR APPLICATION NUMBER: 09/004,306

FRIOR PAPLICATION NUMBER: 09/001-14

FRIOR FILING DATE: 1998-11-0-06

FRIOR FILING DATE: 1998-12-19

FRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 59

FRIOR FILING DATE: 1997-12-19

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Pred. No. 1.8e+02;
1; Mismatches 3; Indels
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      CTHER INFORMATION: MAP TO AL121935.12
CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6
CTHER INFORMATION: EXPRESSED IN PELA, SIGNAL = 4.7
CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9
CTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
CTHER INFORMATION: SWISSFROT HIT: P51684, EVALUE 0.00e+00 US-10-029-386-32911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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ilarity 75.0%; Pred. No. 2.5e+02;
Conservative 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 40, Application US/09774381; Publication No. US20030082677A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           63.6%;
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            232 KYOTUSEPIRW 242
                                                                                                                                                                                                                                                                                                                                                                                          1 KYQQLFEDIRW 11
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US-09-774-381-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497 ELFEDFRW 504
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US-10-029-386-32911

US-10-029-386-32911

Sequence 32911, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CYPTEN TOF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

LENGTH: 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-10-325-430-18
is Sequence 18, Application US/10325430
is Sequence 18, Application US/10325430
is Publication No. US2003015352541
is GENERAL INFORMATION:
is APPLICANT: Millennium Pharmaceuticals, Inc.
is APPLICANT: Silos-Santiago, Inmaculada
is APPLICANT: Risenfeld, Julie Beth
ITILE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
ITILE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
ITILE OF INVENTION: ADPLICATION NUMBER: US/10/325,430
is TILE REFERENCE: MPIO1-294PIRM
is CURRENT FILING DATE: 2002-12-19
is PRIOR FILING DATE: 2001-12-19
is PRIOR FILING DATE: 2001-12-19
is SOFTWARE: PastSEQ for Windows Version 4.0
is SOFTWARE: PastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1920
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-087-192-1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo Sapiens
US-10-325-430-18
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                TYPE: PRT
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5.1.6 Compugen Ltd. GenCore version Copyright (c) 1993 - 2004

using sw model - protein search, OM protein November 10, 2004, 14:52:32; Search time 3.75801 Seconds (without alignments) 281.634 Million cell updates/sec Run on:

US-10-092-750-224 63 Title: Perfect score:

1 KYQQLFEDIRW 11 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	replication licens					hypothetical prote	5		probable sugar tra	hypothetical prote	probable enzyme wi	trehalose operon t	trehalose operon t	hypothetical prote	hypothetical prote	1-phosphatidylinos	1-phosphatidylinos	1-phosphatidylinos	conserved hypothet	5	hypothetical prote	_	귾			nonstructural prot		nonstructural prot	nonstructural prot
SUMMARIES	QI	S56766	S65954	T47223	S64720	C95316	T00339	D69899	JC5068	T14606	S14122	D97161	D95220	B98084	T41158	T14776	A36466	A31317	200666	H81021	E69352	542385	E83241	MNIV2F	MNIVX2	MINIVX4	MNIVX6	MIVX8	MNIVXX	E45539
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	Score	52			20																							36		
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nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	nonstructural prot	NS2 protein - infl
MNIV2	MNIV2A	MNIV2M	MNI V2W	MNIV62	MNI VB1	MNI VB3	MNI VB4	MNIVBS	MNI VB7	MNIVB8	MNI VC2	MNIV26	MNI V2K	MNIVB6	809649
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121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121
57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1
vo	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36
m															

ALIGNMENTS

RESULT 1

replication licensing factor MCM4 - mouse

NyAlternate names: call division cycle control protein CDC21/CDC54

Cipacies: Mus musculus (house mouse)

Cipacie: 13.4Mg-1999 #sequence_revision 13.4Mg-1999 #text_change 09-Jul-2004

Cipace: 13.4Mg-1999 #sequence_revision 13.4Mg-1999 #text_change 09-Jul-2004

Cipace: 13.4Mg-1999 #sequence_revision 13.4Mg-1999 #text_change 09-Jul-2004

RyKimura, #1. Takizawa, N.; Nozaki, N.; Sugimoto, K.

Nucleic Acids Res. 23, 2097-2104, 1995

A; Ritle: Molecular cloning of cDNA encoding mouse Cdc21 and CDC46 homologs and characteris and center number: SS6766

A; Reference number: SS6766

A; Residues: SS6766

A; Residues: 1-862 * KINA

82.5%; Score 52; DB 1; Length 862; 100.0%; Pred. No. 0.33; tive 0; Mismatches 0; Indels Query Match

Local Similarity 100. Les 10, Conservative 1 KYQQLFEDIR 10 Best Loca Matches ò

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818 KYÇQLFEDIR 827

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RESULT 2

replication licensing factor MCM4 - human
replication licensing factor MCM4 - human
replication licensing factor MCM4 - human
replication licensing factor MCM4 - human
NyAlternate names: cell division cycle control protein CDC21/CDC54; S. cerevisiae minich;
Species: Homo sapiens (man)
Cjacte: 13-Aug-1999 #sequence revision 13-Aug-1999 #text_change 09-Jul-2004
CjAccession: S6554; S43199; S44622
R,Musahl, C.; Schulte, D.; Burkhart, R.; Knippers, R.
Eur. J. Biochem. 230, 1096-1101, 1995
A,Title: A human homologue of the yeast replication protein Cdc21. Interactions with othe A,Title: A human homologue of the yeast replication protein Cdc21. Interactions with othe A,Title: A human homologue of the yeast replication protein Cdc21. Interactions with othe A,Tateus: mcdecession: 865954
A,Tateus: mcleic acid sequence not shown
A,Molecule type: mRNA
A,Residues: 'IRHERVATSSASGRLPRNARRRGRALARSBRERPRCGAGGGSREAGPARACPCRAGTPSI', 1-863 <MUS>
A,Cross-references: UNIPROT:P33991; EMBL:X74794; NID:g683749; PIDN:CRA52801.1; PID:g9405: R,Hu, B.

submitted to the EMBL Data Library, August 1993 A;Reference number: S43198 A;Accession: S43198

A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 'ARE',440-636 <HUB2>

A; Accession: S41622

A;Gene: GDB:MCM4; CDC21; CDC54

C; Function:

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AjAccession: C55316
AjStatus: preliminary
AjAccession: C55316
AjStatus: preliminary
AjAccession: C55316
AjStatus: preliminary
AjAccession: C55316
AjStatus: preliminary
AjResidues: 1-266 «KUR»
AjCross-references: UNIPROT: Q92ZMO; GB:ABO06469; PIDN:AAK65093.1; PID:g14523529; GSPDB:GP
AjExperimental source: Errain. D121, meagaplasmid pSymA
AjExperimental source: Errain. D121, meagaplasmid pSymA
BjGalibert, F.; Finan, T.M.; Long, S.R.; Pulner, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hymann, R.W.; Jones, T.
Science 293, 668-672, 2001
AjAuthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
AjAuthors: Kahn, D.; Andembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
AjTitle: The composite genome of the legume symbiont Sinorhizobium meliloti.
AjReference number: Aj6039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                      A) Residues: 1-863 (COU)

A) Residues: 1-863 (COU)

A) Residues: 1-863 (COU)

A) Cross-references: UNIROR: 190664; EMEL: U29178; NID: 91002597; PIDN: AAB01680.1; PID: 91007

A) Cross-references: UNIROR: 190664; EMEL: U29178; NID: 91002597; PIDN: AAB01680.1; PID: 91007

A) Richert A, Maundrell, K.; Kearsey, S.E.

B; Coxon, A.; Maundrell, K.; Kearsey, S.E.

A) Rocles (A) Acids Res. 20, 5711-577, 1992

A) Richer E isslon yeast cdc21(+) belongs to a family of proteins involved in an early step A) Reference number: S26640; MUID: 93087163; PMID: 1454522

A) Accession: S26643

A) Accession: S26643

A) Residues: 513-523, YY, 525-538, 'G', 540-553, 'G', 555-588 (COX)

A) Residues: 513-523, YY, 525-538, 'G', 540-553, 'G', 555-588 (COX)

C) Cromment: The complex of six MCM proteins is one of several proteins that must be bound phosphorylated and dissociate from the chromatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: part of the replication licensing system that permits DNA replication to C;Superfamily: replication licensing factor MCM4; MCM homology C;Keywords: cell cycle control; DNA replication initiation; heterohexamer; nucleus; phosf F;271-764/Domain: MCM homology <MCM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable ABC transporter, permease protein SMa0802 [imported] - Sinorhizobium meliloti (c) Species: Sinorhizobium meliloti (c) Species: Sinorhizobium meliloti (c) Species: Sinorhizobium meliloti (c) Abdres: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 (c) Accession: C95316 (c) Accession: C95316 (c) Abdres: T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse (c) Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. US.A. 98 , 988, 2001 (a) Ajfille: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti A; Reference number: A95262; MUID:21396509; PMID:11481432
C;Date: 13-Aug-1999 #sequence revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: S64720; S26643; S25529
S;Coue, M; Kearsey, S.E.; Mechali, M.
EMBO J. 15, 1085-1097, 1996
A;Title: Chromatin binding, nuclear localization and phosphorylation of Xenopus cdc21 ark
A;Reference number: S64720; MUID:96183193; PMID:8605878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: cdc21
C;Complex: The predominant form is a heterohexamer of MCM2, MCM3, MCM4, MCM5, MCM6, and
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C;Superfamily: spermidine/putrescine transport system permease protein potI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA
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Best Local Similarity 90.0
Matches 9; Conservative
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MCM2 (PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: EMBL:X74794
C;Comment: The complex of six MCM proteins is one of several proteins that must be bound
Phosphorylated and dissociate from the chromatin.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Description: part of the replication licensing system that permits DNA replication to C, Superfamily: replication licensing factor MCM4; MCM homology C, Keywords: cell cycle control; DNA replication initiation; heterohexamer; nucleus; phos F;271-764/Domain: MCM homology <MCM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GDB:433798
C;Complex: The predominant form is a heterohexamer of MCM2, MCM3, MCM4, MCM5, MCM6, and
                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 'ARE', 440-702 <HUB1>
A;Cross-references: EMB1.374794
R;Hu, B.; Burkhart, R.; Schulte, D.; Musahl, C.; Knippers, R.
Nucleid, Acids Res. 21, 5289-5293, 199
Nucleid, Acids Res. 21, 5289-5293, 199
A;Reference number: S41622; MUID:94089373; PMID:8265339
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KYQQLFEDIR 828

1 KYQQLFEDIR 10

à Db

Best Loc Matches

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-858 <KUB>

Query Match
Best Local Similarity 90.0
Matches 9; Conservative

Function:

814 KYĞQLFEDLR 823

RESULT 4

1 KYQQLFEDIR 10

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Score 42; DB 2; Length 266; Pred. No. 5.7;
                                            66.7%;
70.0%;
                                               Query Match
Best Local Similarity
S64720 replication licensing factor MCM4 - African clawed frog N;Alternate names: cell division cycle control protein CDC21/CDC54 C;Species: Xenopus laevis (African clawed frog)
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Gaps

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Indels

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Mismatches

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7; Conservative

Matches

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Gracesin-coupled receptor CKR-i3 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: JC5068
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys Res. Commun. 227, 846-853, 1996
A;Itle: Molecular cloning and RNA expression of two new human chemokine receptor-like gs
A;Attle: Molecular cloning and RNA expression of two new human chemokine receptor-like gs
A;Accession: JC5068
A;Molecule Lype: DNA
A;Residuae: 1-389 < CABA
A;Residuae: 1-389 < CABA
A;Residuae: 1-389 < CABA
A;Residuae: 1-389 < CABA
A;Cross-references: ENBL:Z79784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
C;Comment: This protein belongs to the family of alpha chemokine receptors.
C;Genetics:
A;Gene: GDB:GXYBRE6; STRL22; GRR29; CCR6; CKR-L3; GPR-CY4
A;Cross-references: GDB:570639; OMIN:601835
A;Gene: GDB:GXYBRE6; STRL22; GRR29; CCR6; CKR-L3; GPR-CY4
A;Cross-references: Gprotein-coupled receptor; transmembrane predicted <TM1>
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate status predicted <TM2>
F;73-99/Domain: transmembrane #status predicted <TM3>
F;15-1233/Domain: transmembrane #status predicted <TM3>
F;160-180/Domain: transmembrane #status predicted <TM3>
F;222-233/Domain: transmembrane #status predicted <TM6>
F;222-233/Domain: transmembrane #status predicted <TM6>
F;222-2315/Domain: transmembrane #status predicted <TM7>
F;222-2315/Domain: transmembrane #status predicted <TM6
F;222-2315/Do
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C;Species: Beta vulgaris (beet)
C;Species: Beta vulgaris (beet)
C;Species: Beta vulgaris (beet)
C;Species: Beta vulgaris (beet)
C;Cpate: 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14606; T14617
R;Chiou, T.J.; Bush, D.R.
Plant Physiol. 110, 511-520, 1996
A;Title: Molecular cloning, immunochemical localization to the vacuole, and expra A;Reference number: 218131; MUID:96331183; PMID:874232
A;Accession: T14606
A;Reference number: Z18131; MUID:96331183; PMID:874232
A;Accession: T14606
A;Molecule type: mRNA
A;Residues: 1-549 <CH1>
A;Accession: T14617
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T14617
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T14617
A;Status: Breliminary; translated from GB/EMBL/DDBJ
A;Accession: T14617
A;Status: Breliminary; translated from GB/EMBL/DDBJ
A;Accession: T14617
A;Cross-references: EMBL:U64903; NID:g1778094; PID:g1778095
C;Genetics:
A;Note: BvcDNA-205; BvcDNA-397
C;Superfamily: glucose transport protein
C;Keywords: sugar transport
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Pred. No. 28;
1; Mismatches 3; Indels
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Pred. No. 44;
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63.6%;
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Best Local Similarity 75.0.
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195 KYQTVSEPIRW 205
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nes 7; Conserv
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Matches
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T00339
hypothetical protein KIAA0572 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Ol-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00339
R;Nagase, T: IShikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A;Accession: T00339
A;Title: Prediction of the Coding sequences of unidentified human genes. IX. The complet A;Accession: T00339
A;Molecule type: mRNA
A;Accession: T00339
A;Molecule type: mRNA
A;Residues: 1-1872 «NAG>
A;Cross-references: UNIRROT:O60318; EMBL;AB011144; NID:g3043667; FIDN:BAA25498.1; PID:g3
A;Experimental source: brain; clone HH2391
C;Genetics:
A;Note: KIAA0572
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D69899
conserved hypothetical protein yobM - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Broin, S; Brouillet, S; Bruschi, C;V; Caldwell, B; Capuano, V; Catter, N.M.; Changer, S; Bruschi, C; Ferrari, E.
Nature 390, 249-256, 1997
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A;Experimental source: strain 168
C;Genetics:
A;Gene: yobM
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Pred. No. 1.1e+02;
1; Mismatches 3; Indels
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Pred. No. 11;
1; Mismatches 1; Indels
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77.8%;
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Best Local Similarity 77.00.
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Best Local Similarity 60.0
Matches 6; Conservative
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2 YOOLFEDIRW 11
                                                                        56 YQELLEDPRW 65
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trehalose operon transcription repressor [imported] - Streptococcus pneumoniae (strain R6 C, Species: Streptococcus pneumoniae C, Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C, Accession: B98084 A, Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Ese, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; McY, P.; Sun, P.M.; Winkler, M.E.
A; Dacteriol. 183, 5709-5717, 2001
A,Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A,Accession: B98084
                                                 C; Accession: D95220

C; Accession: D95220

No. (1) (Not Not No. (1) (Not No. (1) (Not No. (1) (No. (1
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-236 «KUR»
A;Residues: 1-236 «KUR»
A;Exper-references: UNIPKOT:Q97NW8; UNIPROT:Q8DNI5; GB:AE005672; PIDN:AAK75957.1; PID:g14
A;Exper-imental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1.310 <HIL>
A;Cross-references: UNIPROT:074865; EMBL:AL031907; PIDN:CAA21429.1; GSPDB:GN00068; SPDB:C;A;Cross-references: strain 972h-; cosmid cl8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1.236 «KUR»
A;Cross-references: UNIPROT:Q97NW8; UNIPROT:Q8DNI5; GB:AE007317; PIDN:AAL00503.1; PID:g1:
C;Genetics:
A;Gene: treR
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03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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R,H11bert, H, Ducsterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, submitted to the EWBL Data Library, October 1998
A;Reference number: Z21973
A;Recession: T41158
A;Status; preliminary; translated from GB/EWBL/DDBJ
A;Rolecule type: DNA
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26;
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Pred. No. 26;
2; Mismatches
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Pred. No. 26;
2; Mismatches
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Matches 7; Conserv
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Best Local Si
Matches 7;
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:P41248; EMBL:X57669; NID:g450343; PIDN:CAA40864.1; PID:g4438
A;Cross-references: UNIPROT:P41248; EMBL:X57669; NID:g450343; PIDN:CAA40864.1; PID:g4438
R;Spassova, M.; Moneger, F.; Leaver, C.J.; Petrov, P.; Atanassov, A.; Nijkamp, H.J.J.; H
Biol. 26, 1819-1831, 1994
A;Title: Characterisation and expression of the mitochondrial genome of a new type of cy
A;Reference number: S52010; MUID:95161706; PMID:7858220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable enzyme with a TIM-barrel fold (imported) - Clostridium acetobutylicum ("Species: Clostridium acetobutylicum ("Species: Clostridium acetobutylicum ("Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 ("Sacession: D97161 "Breton, O", Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, "S. Nolling, O.; Breton, O.; Mondin, B.V.; Smith, D.R. "Bacteriol. 183, 4823-4838, 2001 "Breton, O", Smith, D.R. "Affiles Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cloby. A. "Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:097H92; GB:AE001437; PIDN:AAK80079.1; PID:g15025111; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                      C;Date: 16-Sep-1992 #sequence revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: S14122; S52011; S48855
Cyrr. Genet. 18, 1950
A;Title: The Cytochrome oxidase subunit III gene in sunflower mitochondria is cotranscri A;Reference number: S14122; MUID:91070622; PMID:2174745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trafalose operon transcription repressor [imported] - Streptococcus pneumoniae (strain C; Species: Streptococcus pneumoniae
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C;Keywords: mitochondrion
F;l-85/Domain: H+-transporting ATP synthase alpha chain homology (fragment)
                                                                                                                                nypothetical protein B (COXIII 5' region) - common sunflower mitochondrion C;Species: mitochondrion Helianthus annuus (common sunflower)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-159 <SPA>
A;Cross-references: EMBL:X82386; NID:g563544; PIDN:CAA57787.1; PID:g563546
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Pred. No. 17;
1; Mismatches 3; Indels
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C,Superfamily: conserved hypothetical protein HI0090
                                                                                                                                                                             C; Species: mitochondrion Helianthus annuus (common
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Pred. No. 24;
3; Mismatches
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Best Local Similarity 45.5%;
Matches 5; Conservative
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KYDEMNSDVRW
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Best Local Similarity
Matches 6; Conserv
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A Molecule type: DNA
A Residues: 1-221 <KUR>
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RESULT 12

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RESULT 15
T14776
hypothetical protein DXF2p434N101.1 - human (fragment)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C.Accession: T14776
R.Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
A.Reference number: Z18183
A.Reference number: Z18183
A.Accession: T14776
A.Status: preliminary
A.Mccession: T14776
A.Status: preliminary
A.Mcessidues: 1-629 < POU-
A.Cross_references: UNIPROT: Q9UFY1; EMBL: All10247
A.Experimental source: adult testis; clone DKFZp434N101
C.Genetics: DKFZp434N101.1
C.Superfamily: 1-phosphatidylinositol-4.5-bisphosphate phosphodiesterase II; 1-phosphatihodiesterase domain Y homology; SH2 homology; SH3 homology
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                                                                                                               Query Match 60.3%; Score 38; DB 2; Length 310; Best Local Similarity 66.7%; Pred. No. 35; Matches 6; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                            1 KYQQLFEDI 9
|| |:|||:
22 KYSQVFEDV 30
A;Gene: SPDB:SPCC18.15
A;Map position: 3
A;Introns: 59/2
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Search completed: November 10, 2004, 15:55:08 Job time : 4.75801 secs

1 KYQQLFEDIR 10 | | | | | | | 538 RYQQPFEDFR 547

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OM protein - protein search, using sw model

November 10, 2004, 14:50:40; Search time 18.4377 Seconds (without alignments) 343.270 Million cell updates/sec Run on:

US-10-092-750-224 63 1 KYQQLFEDIRW 11 Title:
Perfect score:
Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P49717 mus musculu	mus	SUM:	mus	78 mus	homo	Q8nehl homo sapien	08 hor	xenopus	P30664 xenopus lae	Q6g141 xenopus tro	Q6nzv2 brachydanio	LC)	_		Q92zm0 rhizobium m		н	photorhabd	_	_	Q82sd9 nitrosomona	Q6pjp6 homo sapien	Aah13285 homo sapi	Q938k3 temperate p	streptococ		stre	8 homo sa	300 hon	034377 bacillus su
SUMMAKIES	QI	MCM4 MOUSE	Q8C1 <u>Z</u> 0	Q9D077	Q921D5	BAC40578	MCM4 HUMAN	QBNEH1	AAS83108	042589	MCM4 XENLA	Q6GL41	Q6NZV2	AAH65958	Q975L8	Q7MA20	Q92ZM0	Q834N6	Q7QMZ1	O7N8Q5	Q6EB27	092421	Q82SD9	Qepabe	AAH13285	Q938K3	Q8K6Q1	Q8NZS4	O9AON0	MC3A_HUMAN	389	034377
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	Length	862	862	862	862	862	863	863	863	858	863	863	845	845	911	200	266	486	125	110	286	302	705	778	778	9	80	9	9	1980	98	9
æ	Query Match	82.5	82.5	82.5	ά.	82.5	82.5	82.5	82.5	٠	79.4	79.4	74.6	74.6	71.4	69.8	66.7	66.7	65.1	m	63.5	۳,	ω.	63.5	m.	•	ë.	63.5	m	63.5		61.9
	Score	52	52	52	52	52	52	52	52	20	20	20	47	47	45	44	42	42	41	0.4	40	40	40				40	40	40	40	40	39
	Result No.		0	٣	4	w	9	7	60	ი	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Q6mnm4 bdellovibri Cae79127 bdellovib P5184 home sapien Q6cpj4 kluyveromyc P93076 beta vulgar Q7rkf0 plasmodium Q8ztr7 pyrobaculum Q8ztr7 pyrobaculum Q8dni5 streptococc Q97nw8 streptococc Q97nw8 streptococc Q97nw8 streptococc Q97nw8 streptococc	
Q6MNM4 CAE79127 CKR6 HUMAN Q6CPJ4 P93075 P93075 Q7RKF0 Q8ZTT7 YM19 HELAN YM19 HELAN Q97HJ2 Q9DN15 Q9DN15 Q6W249	
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ALIGNMENTS

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PRINTS; PRO1657; MCMFAMILY.
PRINTS; PRO1660; MCMPROTBIN4.
PRODOM; PDO01041; MCM; 1.
SMART; SM00350; MCM; 1.
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Best Local Similarity 100.
Matches 10, Conservative
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Q9D077
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STRANTE-CIH; TISSUE=Brain;
The FANTOM COnsortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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SEQUENCE FROM N.A.
STRAIN=C3H; TISSUE=Brain;
MEDLINE=C3H; TISSUE=Brain;
MEDLINE=C499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus brain CRL-143 BC3H1 cDNA, RIKEN full-length enriched
library, clone:6430050M09 product:mini chromosome maintenance
deficient 4 homolog (S. cerevisiae), full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C3H; TISSUE=Brain,
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                               ;
PROSITE; PS500847; MCM 1; 1.
PROSITE; PS50051; MCM-2; 1.
Transcription regulation. DNA-binding; Nuclear protein; DNAIN 457 666 MCM.
                                                                                                                                                                                                                                82.5%; Score 52; DB 1; Length 862; 100.0%; Pred. No. 1.5; tive. 0; Mismatches 0; Indels
                                                                                                                   509 516 ATP (Potential).
530 530 Q -> R (in Ref. 2).
572 1 -> T (in Ref. 2).
862 AA, 96736 WW, 516ACCIA3C6FB16E CRC64;
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MEDLINE=9927953; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
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Best Local Similarity 100.0
Marches 10; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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NP BIND
CONFLICT
                                                                                                                                                                                      SEQUENCE
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annoctation update)
Mus musculus 10 days embryo whole body CDNA, RIKBN full-length
enriched library, clone:2510042115 product:mini chromosome maintenance
deficient 4 homolog (S. cerevisiae), full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Rawai J. "RIEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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0
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100.0%; Pred. No. 1.5;
ive 0; Mismatches 0; Indels
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PROSITE; PS50051; MCM 2; 1.
SEQUENCE 862 AA; 96752 MW; FF2FA597021EB8E6 CRC64;
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862 AA; 96764 MW; 6533BD3FA75A7866 CRC64;

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SQ SEQUENCE
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RP SCUENCE FROM N.A.

RP STRATN=CS7BL/60; TISSUE=Whole body;

RAdachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

Arakawa T., Bono H., Carninci P., Fukuda S., Pukunishi Y., Furuno M.,

Arakawa T., Bono H., Carninci P., Fukuda S., Pukunishi Y., Furuno M.,

Arakawa T., Ishii Y., Itoh M., Itzawa M., Kato H.,

Rawai J., Kojima Y., Konno H., Koya S., Kurihara C.,

Rawai J., Kojima Y., Konno H., Koya S., Kurihara C.,

Rawai J., Kojima Y., Konno H., Salto R., Bakai K., Onno M.,

Razaki Y., Okido T., Okido T., Owa C., Saito H., Salto R., Sakai T.,

Razaki Y., Okido T., Yamamura T., Yahinagwa A., Shiraki T.,

Sano H., Sasaki D., Shibaca K., Shibata Y., Shinagwa A., Shiraki T.,

Sano H., Sasaki D., Shibaca K., Shibata Y., Shinagwa A., Shiraki T.,

Sano H., Sasaki D., Shibaca K., Shibata Y., Shinagwa A., Shiraki T.,

Sano H., Sasaki D., Shibaca K., Shibata Y., Shinagwa A., Shiraki T.,

Sano H., Sasaki D., Shibaca K., Shibata Y., Shinaki E.,

Rubmitted (ULL-2000) to the EWBI/GenBank/DDBJ databases.

BRD, AKO11741; BAB27813.1; -.

BRD, GO:00005634; Finucleus; IEA.

GO: GO:0005634; Finucleus; IEA.

GO: GO:0005634; Finucleus; IEA.

GO: GO:0005634; Finucleus E.

BRD, AMA AND Adependent ATPase activity; IEA.

GO: GO:0005637; Finucleus E.

BRD, RIPEPPO: IPRO0355; CytC_heme_BS.

InterPro: IPRO0355; CytC_heme_BS.

InterPro: IPRO0355; CytC_heme_BS.

InterPro: IPRO0355; CytC, Pume_BS.

InterPro: IPRO0355; MCM; 1.

BRANTS; PRO1660; MCM; 1.

BRANTS; PRO1660; MCM; 1.

BRANTS; PRO1660; MCM; 1.

BROSITE; PRO0350; MCM; 1.
                                                                                                                                                                                [3]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM CONSORTIUM,
The FANTOM CONSORTIUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C5/BL/6J; TISSUE=Whole body;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CTSPEL/G4; TISSUE=whole body;
STRAIN-CTSPEL/G4; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konnon H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watsuhiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Rokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RIKIN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
STRAIN=CS7BL/6J; TISSUE=Whole body; MEDLINE=2108560; PubMed=11217851; RIKEN FANTOM CONSORTIUM; RIKEN FANTOM CONSORTIUM; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Straubenger R.;
Straubenger R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013094; Mar4.

MGD; MGI:1031999; Mcm4.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:DNA-dependent ATPase activity; IEA.

GO; GO:000166; F:Nucleotide binding; IEA.

GO; GO:000166; F:Nucleotide binding; IEA.

GO; GO:000166; F:Nucleotide binding; IEA.

GO; GO:000167; P:Nucleotide binding; IEA.

GO; GO:000167; P:Nucleotide binding; IEA.

InterPro; IPR003593; AAA ATPASE.

InterPro; IPR00345; CytCheme_BS.

InterPro; IPR00494; MCM.

Pfam; PF00493; MCM; 1.
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TISSUS=Mammary tumor. Metallothionien-TGF alpha model. 10
virgin mouse. Taken by biopsy.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              0921D5 PRELIMINARY; PRT; 862 AA. 0921D5; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DAR-2004 (TrEMBLrel. 26, Last annotation update) Minichrosome maintenance protein 4.
    82.5%; Score 52; DB 2; 100.0%; Pred. No. 1.5; cive 0; Mismatches
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PRINTS; PRO1660; MCMPROTEIN4
ProDom; PD001041; MCM; 1.
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Query Match
Best Local Similarity 100.
Matches 10; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22054683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
whallyels of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NOD; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                   BAC40578;
14-APR-2004 (TrENBLrel. 27, Created)
14-APR-2004 (TrENBLrel. 27, Last sequence update)
14-APR-2004 (TrENBLrel. 27, Last sequence update)
2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E450026E21 product:mini chromosome maintenance deficient 4 homolog (S. cerevisiae), full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEGUENCE FROM N.A.
SYRINI-NOD; TISSUB-Thymus;
MEDLINE-20530913; PubMed=11076861;
Shibata K., Icoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                 .
0
                                                                                                                                             Length 862;
                                                                                                                                                                                 0; Indels
                                                                                                         862 AA; 96719 MW; 516ACA3C8BF7EE3E CRC64;
                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                           862 AA.
                                                                                                                                                                               0; Mismatches
SMART; SM00382; AAA; 1.

PROSTITE; PRO01360; MCM; 1.

PROSTITE; PS001400; CYTOCHROME_C; UNKNOWN_1.

PROSTITE; PS000847; MCM_1; 1.

PROSTITE; PS50051; MCM_2; 1.

ATP-bind PS50051; MCM_2; 1.

SEQUENCE 862 AA; 96719 MW; 516ACA3C8BF
                                                                                                                                             Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                         PRT;
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                             82.5%; 8
                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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MEDLINE=97430835; PubMed=9284934;
Ladenburger E.M., Fackelmayer F.O., Hameister H., Knippers R.;
"MCM4 and PRKDC, human genes encoding proteins MCM4 and DNA-PKcs, are
close neighbours located on chromosome 8q12-->q13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hu B., Burkhart R., Schulte D., Musahl C., Knippers R.;
"The Pl family: a new class of nuclear mammalian proteins related to the yeast Mcm replication proteins.";
Nucleic Acids Res. 21:5289-523(1989).
-!- FUNCTION: Involved in the control of DNA replication.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the MCM family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Connelly M.A., Zhang H., Kieleczawa J., Anderson C.W.; "The promoters for human DNA-PKCs (PRKDC) and MCM4: divergently transcribed genes located at chromosome 8 band q11."; Genomics 47:71-83(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKRI integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.", Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                82.5%; Score 52; DB 2; Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Submitted (FBB-1995) to the EMBL/GenBank/DDBJ databases.
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TISSUE-Cervix;
MEDLINE-94089373; PubMed-8265339;
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Similarity 100.
10; Conservative
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AAS83108;
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDINE-22388257; PubMed=12477932;

MEDINE-22388257; PubMed=12477932;

MEDINE-22388257; PubMed=12477932;

MIDINE-22388257; PubMed=12477932;

Marsaer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

Hopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Haish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Minichromosome maintenance protein 4 (MCM4 minichromosome maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00847; MCM 1; 1.
PROSITE; PS50051; MCM 2; 1.
ATP-binding; DNA replication; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.5%; Score 52; DB 1; Length 863; 100.0%; Pred. No. 1.5; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             458 667 MCM.

510 517 ATP (Potential).

62 62 T -> P (in Ref. 2).

506 506 M -> L (in Ref. 2).

650 650 M -> L (in Ref. 2).

863 AA; 96610 NW; 50010575C41BA90C CRC64;
                                                                                                                                                                                               MIM; 602633; C: nucleus; NAS. GO; GO:0005634; C:nucleus; NAS. GO; GO:0005634; F:ATP binding; NAS. GO; GO:0005564; F:ATP binding; NAS. GO; GO:0005260; P:DNA replication; NAS. InterPro; IPR001209; MCM. InterPro; IPR001209; MCM. InterPro; IPR001209; MCM; I. PRINTS; PR01660; MCMPADILY. PRINTS; PR01660; MCMPROTEIN4. PRINTS; PR01660; MCMPROTEIN4. SMART; SMO0322; AAA; I.
                                                                                                                 EMBL; X74794; CAA52801.1; -.
EMBL; 056360; AAC52018.1; -.
EMBL; U90415; AAC55123.3; -.
PIR; S65954; S65954.
Genew; HONC:6947; MCM4.
Reactome; P33391; -.
MIM; 602638; -.
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Name=MCM4;
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NP BIND
CONFLICT
CONFLICT
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SEQUENCE FROM N.A.

Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,

Rayon C.P., Mayuyen D.A., Poel C.L., Robertson D.D., Schackwitz W.S.,

Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;

Rayling, Axs88245; AA810811; --

Rembl, Axs88245; AA831081; --

Roj, Go:0005524; E:ATP blinding; IEA.

GO; GO:0005634; E:DNA-dependent ATPasse activity; IEA.

GO; GO:0001675; F:NAN Arphase.

Roj, GO:00010169; F:DNA-dependent ATPasse activity; IEA.

GO; GO:000101619; F:DNA-dependent ATPasse activity; IEA.

GO; GO:000101619; M.M.

ROJ, GO:000101619; M.M.

InterPro; IPRO08047; M.M.

PRINTS; PRO1665; MCMPROTEIN4.

PROSTIE; PRO1661; MCM; 1.

RRATT; SMO0382; AAA; 1.

RRATT; SMO0382; AAA; 1.

RRATT; SMO0382; AAA; 1.

RRATT; SMO0381; MCM; 1.

RRATT; SPSIOS1; MCM; 1.
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gabbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S., Krzywinski M.I., Skalska U., Schmutz J., Myers R.W., Butterfield Y.S., Jones S.J., Marra M.A., Green E.D., Dickson M.C., Schein J.E., Jones S.J., Marra M.A., Pullal analysis of more than 15,000 full-length human and mouse cDNA sequences."
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Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
Mayyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.
Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutberia; Primates; Catarrhini; Hominidae; Homo.
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
MCM4 minchromosome maintenance deficient 4 (S. cerevisiae).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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AAS83108
AC AAS8
DT 14-A
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CO Buka
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                                                                                                                                        Gaps
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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MCM4 XENLA
DI — MCM4 XENLA
STANDARD; PRT; 863 AA.

AC P30664; 091679;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-CT-1996 (Rel. 34, Last sequence update)
DT 05-UUL-2004 (Rel. 44, Last annotation update)
DE DNA replication licensing factor MCM4 (CDC21 homolog) (P1-CDC21)
DE X.MCM4).
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                                                                                         DB 2; Length 863; 1.5;
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                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins in Xenopus eggs.";

EMBO 1. 16:3320-3331(1997).

EMBO 1. 16:3320-3331(1997).

R PIR; T47223; T47223.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005274; F:DNA binding; IEA.

GO; GO:000547; F:DNA binding; IEA.

GO; GO:000647; F:DNA-dependent ArPase activity; IEA.

GO; GO:000670; P:DNA-replication initiation; IEA.

InterPro; IPR003593; AAA, ArPase.

InterPro; IPR001208; MCM.

InterPro; IPR001208; MCM.

InterPro; IPR003047; MCM.

InterPro; IPR003047; MCM.
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS88245; AAS83108.1; -.
SEQUENCE 863 AA; 96575 MW; 6D79DA81DD980BAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             858 AA; 97053 MW; DACBFAC72943AF34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          858 AA.
                                                                                         82.5%; Score 52; DB
100.0%; Pred. No. 1.5
:ive 0; Mismatches
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PRINTS; PR01660; MCMPROTEIN4.
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SMART; SM00382; AAA; 1.
SMART; SM00350; MCM; 1.
                                                                           Query Match
Best Local Similarity 100.
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Matches 9; Conservative
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                                                                                                                                                                                                                         819 KYQQLFEDIR 828
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NCBI_TaxID=8355;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILIDES 961831919; PubMed=8605878;
MEDILIDES 961831919; PubMed=8605878;
Coue M., Kearsey S.E., Mechali M.;
"Chromotin binding, nuclear localization and phosphorylation of
"Chromotin binding, nuclear localization and associated with the control
of initiation of DNA replication.";
EMBO J. 15:1085-1097(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJNE=97057222; PubMed=8901561;
Hendrickson M., Madine M., Dalton S., Gautier J.;
"Phosphorylation of MCM4 by edc2 protein kinase inhibits the activity
of the minichromosome maintenance complex.";
Proc. Natl. Acad. Sci. U.S.A. 93:12223-12228(1996).
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MEDLINE=93087163; PubMed=1454522;
MEDLINE=93087163; PubMed=1454522;
Coxon A., Maundrell K., Kearsey S.E.;
"Fission yeast cdc21+ belongs to a family of proteins involved in legisly step of chromosome replication.";
Nucleic Acids Res. 20:5571-5577(1992).
-i- FUNCTION: Involved in the control of DNA replication.
-i- SUBCELLULAR LOCATION: Nuclear (By similarity).
-i- SIMILARITY: Belongs to the MCM family.
Xenopus láevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amplibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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ATP (Potential).
ATP (in Ref. 2).
RA -> LS (in Ref. 2).
9A47003097EEDE2E CRC64;
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819 KYQQLFEDLR 828

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                   TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.68;
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PRINTS; PR01660; MCMPROTEIN4
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TISSUE=Embryo;
                                                                                                             NCBI_TaxID=7955;
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X MEDLINE=2238627; PubMed=12477332;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Alusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Aluschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

A Diacchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,

A Diacchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,

B Diacchenko L., Marusina W., Forence A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Workernan K.J., Maramon R.D., Mullahy S.J.,

R. Boaks S.A., McEwan P.J., McKernan K.J., Maramon R.D., Hulyk S.W.,

R. Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Pahey J., Helton E. Ketteman M., Madan A., Rodigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Dheychenko Y., Bouffard G.G.,

M. Mitting M., I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Rotyminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,

R. "Generation and initial analysis of more than 15,000 full-length human
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                                                                        US-UUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota: Mestern clawed frog) (Silurana tropicalis).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO4670; AMTH4670.1; -.
InterPro; IPR0040208; MCM.
InterPro; IPR00403; MCM.
IPRINTS; PR01660; MCMPANILY.
PRINTS; PR01660; MCMPROTEIN4.
IPRODOM; PD001041; MCM; 1.
IPROSITE; PS00847; MCM.; 1.
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REQUENCE 863 AA; 97195 MW; 2AAFF32FE85BE97B CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 2;
Pred. No. 3.4;
1; Mismatches
                                            863 AA
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Name=mcm4;
Brachydanio rerio (Zebrafish) (Danio rerio).
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                                        PRELIMINARY,
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Best Local Similarity
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                                    Q6GL41;
Q6GL41;
05-JUL-2004 (
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QGNZV2
ID QGNZVA
AC QGNZV
DT 05-JU
DT 05-JU
DT 05-JU
DE MCMM
IGN NAMM
OS Brach;
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.P., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hisheh F.,

Bartchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villadon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Locuman M., Sodergren E.J., Lu X., Gibbs R.A.,

A Niting M., Madan A., Young A.C., Shecknerko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse CDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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02-MXR-2004 (TrEMBLrel. 27, Last sequence update)
02-MXR-2004 (TrEMBLrel. 27, Last annotation update)
02-MXR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Brachydamio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, panio.
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Pred. No. 12;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BEO66598; AAH65958.1; -
InterPro; IPR001593; AAA_ATPase.
InterPro; IPR001208; MCM.
InterPro; IPR00147; MCM.
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SWART; SM00382, AAA; 1.
PROSITE; PS00847; MCM 1; 1.
PROSITE; PS50051; MCM 2; 1.
SRATP-binding.
SEQUENCE 845 AA; 94523 MW; 8D959D2C956A63DA CRC64;
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Best Local Similarity
Matches 8; Conserv
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Q7MA20
8
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          Attausher R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altachine F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachil S.F., Zeeberg B. Duetow K.H., Schaefer C.F., Bhat N.K.,

Altachil S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Bosak S.A., McKwam P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

"T "Generation and initial analysis of more than 15,000 full-length human

"T "Forc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=21456156; PubMed=11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshisawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain?.";

DNA Res. 38:123-140(2001).

BNBL, AP000928; BAB65382.1;

GO; GO:0008026; F:ATP binding; IEA.

GO; GO:0008026; F:ATP dependent helicase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR01411645; DBAD/DBAH N.

InterPro; IPR011645; DBAD/DBAH N.

InterPro; IPR011655; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Straubberg R., Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases. EMBL, BC065958; AAH65958.1; -. Hypothetical protein. SEQUENCE 845 AA; 94523 MW; 8D959D2C956A63DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
911aa long hypothetical ATP-dependent helicase.
OrderedLocusNames=$70401;
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MEDLINE=22388257; PubMed=12477932;
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Q975L8;
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  RYARA KAARA 
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RAMEDITEREZERS 1889; PubMedate 14500908; RAMEDITEREZERS 1889; PubMedate 14500908; RAMEDITEREZERS 1889; PubMedate 14500908; RAMEDITEREZERS 1880 RAMEDITEREZERS 1880 RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880; RAMED 1880;
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Wolinella.
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                                                                                                                                                                                                                                                      911 AA; 104448 MW; 24B758D9F066200C CRC64;
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
ATP-binding; Complete proteome; Helicase; Hydrolase; Bypothetical protein.
SEQUENCE 911 AA; 104448 MW; 24B758D9F066200C CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2004 (TrEMBLrel. 26, Created)
1-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
ATP SYNTHASE FI ALPHA SUBUNIT (EC 3.6.3.14).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=DSMZ 1740;
MEDLINE=22882897; PubMed=14500908;
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|35 KYRKLFENLKW 145
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465 KYPQIFEDIR 474

Search completed: November 10, 2004, 15:53:37 Job time : 20.5146 secs

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Sequence 53, Appl
Sequence 53, Appl
Sequence 53, Appl
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Sequence 53, Appl
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Sequence 312, Appl
Sequence 18082, Appl
Sequence 18082, Appl
Sequence 332, Appl
Sequence 332, Appl
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Sequence 1714, Appl
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Sequence 48310, A
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143.349 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-997-68-53

US-08-997-362-53

US-08-873-970-53

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US-09-95-63-53

US-09-324-53-53

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US-09-348-681A-7814

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US-08-246-361A-25
US-08-463-772-25
PCT-US93-05000-25
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match 1
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Perfect score:
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44, Appli
4400, Ap
30475, A
18421, A
8, Appli
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7212, App
7, Appli
7, Appli
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31524, A
8001, Ap
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Sequence 33093, Application US/09270767

GARERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

FILE REFERENCE: File Reference: 7356-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 33093

LENGTH: 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-270-767-48310

j Sequence 48310, Application US/09270767

j Sequence 48310, Application US/09270767

j Septemt No. 6703491

j GENERAL INFORMATION:

j APPLICANT: HOMBURGE et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

TITLE OF INVENTION: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 48310

LENGTH: 155

LENGTH: 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 4; Length 155;
Pred. No. 4.5;
3; Mismatches 4; Indels
US-08-460-694-3
US-08-460-744-3
US-07-660-741-3
US-08-193-977-4
US-08-193-977-4
US-09-252-991A-18421
US-08-522-166-8
US-08-488-382A-8
US-08-488-382A-8
US-08-488-382A-8
US-08-488-382A-8
US-08-488-382A-8
US-08-48-117-7
US-08-46-517-7
US-08-46-517-7
US-08-63-61A-7
US-08-63-61A-7
US-08-63-361A-7
US-08-63-361A-7
US-08-63-772-7
US-08-63-361A-7
US-09-63-991A-31524
US-09-63-991A-31524
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; CRGANISM: Drosophila melanogaster
US-09-270-767-48310
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Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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CLASSIPE CATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
LING DATE: JUBE 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: AUGUST 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
                                                                                                ZIP: 98121
COMPUTER REAABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
  ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
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Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 206-269-0563
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MOLECULE TYPE: protein
US-08-997-362-53
                 STREET: Zour
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STATE: WA
COUNTRY: USA
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                                                                             RESULT 3
US-08-53
US-08-97-080-53
Sequence 53, Application US/08997080
Partent No. 596854
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
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Patent No. 5982867
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Wisser, Elizabeth
APPLICANT: Wisser, Elizabeth
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 5.1;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11000.1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet,
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000
TELECOMMUNICATION INFORMATION:
TELECPHONE: 206-269-0565
TELEFAX: 206-269-0563
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27 LGENFEQOMEQLYLA 41
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SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Matches 9; Conservative
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MOLECULE TYPE: protein
US-08-997-080-53
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Sequence 53, Application US/08873970

Patent No. 6001361

GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Visser, Blizabeth
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Stinner, Margot
APPLICANT: Stinner, Margot
APPLICANT: Stinner, Margot
APPLICANT: STORT TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
                                                             Gaps
                                                          ..
0
56.6%; Score 43; DB 2; Length 175; 75.0%; Pred. No. 5.1; 3; Indels ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98121
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEGO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 CITY: Seattle
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Sequence 53, Application US/08705347A Patent No. 6284255 GENERAL INFORMATION:
                                            53:
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INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
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                                            INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
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Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 9; Conservative
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18 GYEFSRACEALY 29
    TELEFAX: 206-269-0563
TELEX:
                                                                                                                                                                                                                                                                                                          2 GEEFSRAAEKLY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GEEFSRAABKLY 13
                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
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STRANDEDNESS: si:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98121
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STATE: WA
COUNTRY:
                                                                                                                                                                                     US-09-095-855-53
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Patent No. 6160093

GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: DISKETTE COMPATIONE
OPERATING SYSTEM: DOS
SOFTWARE: Rescence for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE: 29-40G-1996
APPLICATION NUMBER: 08/73,970
FILING DATE: 29-40G-1997
APPLICATION NUMBER: 08/873,970
FILING DATE: 29-50G-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-50C-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                         11000.1002C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11000.1002c3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43;
Pred. No.
APPLICATION NUMBER: US/08/873,970
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 37,007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                             LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GEEFSRAAEKLY 13
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                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-873-970-53
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US-09-095-855-53
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                                                      Gaps
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APPLICANT: Hiyama, Jun
APPLICANT: Hiyama, Jun
APPLICANT: Hiyama, Jun
APPLICANT: Signer, Flizabeth
APPLICANT: Scott, Linda
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 55
CORRESPONDENCES: 55
CORRESPONDENCES: 55
ANDRESSEE: Speckman Picard PLLC
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
56.6%; Score 43; DB 3; Length 175; 75.0%; Pred. No. 5.1; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 3; Length 175; Pred. No. 5.1; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,347A
FILING DATE: 28-AUG-1996
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REPREBUCE/DOCKET NUMBER: 37,007
REPREBUCE/DOCKET NUMBER: 37,007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 206.269.0563
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                      Sequence 53, Application US/09324542

Patent No. 6328978

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for UNRERY APPLICATION NUMBER: US/09/324,542

CURRENY FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
ENERGY FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ## SPEIGNATION:
## APPLICANT: Wateson, James D.
## APPLICANT: Wateson, James D.
## APPLICANT: Tan, Paul L. J.
## TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections FILE REFERENCE: 11000.1002c4
## CURRENT APPLICATION NUMBER: US/09/205,426
## CURRENT FILING DATE: 1998-06-11
## BARLIER FILING DATE: 1998-06-11
## BARLIER APPLICATION NUMBER: 08/997,362
## BARLIER APPLICATION NUMBER: 08/997,362
## BARLIER FILING DATE: 1997-06-12
## BARLIER FILING DATE: 1997-06-12
## BARLIER FILING DATE: 1997-06-12
## BARLIER FILING DATE: 1996-08-29
## WIMBER OF SEQ ID NOS: 208
## SOFTWARE: FastSEQ for Windows Version 3.0
## SEQ ID NO 53
## LINGHIER FILING DATE: 1996-08-29
## SOFTWARE: FASTSEQ for Windows Version 3.0
## SEQ ID NO 53
## CONTACT OF TANK OF TANK OF TANK ORGANISM: Mycobacterium vaccae
## US-09-205-426-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.6%; Score 43; DB 3; Length 175; ilarity 75.0%; Pred. No. 5.1; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/09205426 Patent No. 6406704 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-200-643-53
; Sequence 53, Application US/09200643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mycobacterium vaccae US-09-324-542-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYEFSRACEALY 29
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Best Local Similarity
Matches 9; Conserv
JS-09-324-542-53
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PRICE APPLICATION NUMBER: USSN 60/141031
PRICE APPLICATION NUMBER: DE 1933145.3
PRICE APPLICATION NUMBER: DE 19331478.0
PRICE PRILING DATE: 1939-07-06
PRICE PRILING DATE: 1939-07-06
PRICE PRILING DATE: 1939-07-06
PRICE PRILING DATE: 1939-07-06
PRICE PRILING DATE: 1939-07-06
PRICE PRILING DATE: 1939-07-06
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PRICE PRILING DATE: 1939-07-06
PRICE PRILING DATE: 1939-07-09
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US-09-602-787A-312
US-09-602-787A-312
| US-09-602-787A-312 |
| Sequence 312, Application US/09602787A |
| Patent No. 669651 |
| GENERAL INFORMATION: |
| APPLICANT: Pompejus, Mark |
| APPLICANT: Sch"der, Hartwig |
| APPLICANT: Sch"der, Hartwig |
| APPLICANT: Calder, Oskar |
| APPLICANT: APPLICANT: APPLICANT: INFORMATION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS |
| TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE |
| TITLE OF INVENTION: TRANSPORT |
| FILE REFERENCE: BG1-125C |
| CURRENT APPLICATION NUMBER: US/09/602,787A |
| CURRENT FILING DATE: 2000-06-23
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Pred. No. 23;
3; Mismatches 4; Indels
   PRICK FILING DATE: 1999-07-09
PRICK APPLICATION NUMBER: DE 19932228.7
PRICK APPLICATION NUMBER: DE 19932229.5
PRICK FILING DATE: 1999-07-09
PRICK FILING DATE: 1999-07-09
PRICK APPLICATION NUMBER: DE 19932230.9
PRICK APPLICATION NUMBER: DE 1993220.3
PRICK APPLICATION NUMBER: DE 1993205.0
PRICK APPLICATION NUMBER: DE 19933005.0
PRICK FILING DATE: 1999-07-14
PRICK APPLICATION NUMBER: DE 19933005.0
PRICK APPLICATION NUMBER: DE 19940765.7
PRICK APPLICATION NUMBER: DE 19940765.7
PRICK APPLICATION NUMBER: DE 19940765.7
PRICK APPLICATION NUMBER: DE 19940765.7
PRICK APPLICATION NUMBER: DE 19940765.7
PRICK APPLICATION NUMBER: DE 19940765.7
PRICK APPLICATION NUMBER: DE 19940765.7
PRICK APPLICATION NUMBER: DE 19940765.7
PRICK APPLICATION NUMBER: DE 19940765.7
PRICK APPLICATION NUMBER: DE 19940831.9
PRICK FILING DATE: 1999-08-27
PRICK APPLICATION NUMBER: DE 1994083.5
PRICK APPLICATION NUMBER: DE 1994083.5
PRICK APPLICATION NUMBER: DE 1994083.5
PRICK PILING DATE: 1999-08-31
PRICK PILING DATE: 1999-08-31
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PRICK PILING DATE: 1999-09-03
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PRICK PILING DATE: 1999-09-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 53.3%;
Matches 8; Conservative
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Sequence 1309, Application US/09538092
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                                                                                                                                                                                                                                                                                                                                 FEATURE:
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-7
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18082
LENGTH: 312
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                                                                  Query Match
56.6%; Score 43; DB 4; Length 713;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 4; Length 312;
Pred. No. 14;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.3%; Score 42; DB 4; Length 324; 53.8%; Pred. No. 15; tive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                           Sequence 18082, Application US/09252991A Patent No. 6551795
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-787A-312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18082
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365 VSEEIAREVEKLFLA 379
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Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                      1 IGEEFSRAAEKLYLA 15
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21 QSFTKAAEKLFIA 33
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Best Local Similarity 53.8
Matches 7; Conservative
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29 FSRAAERLFVA 39
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US-09-252-991A-18082
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RESULT 15 US-09-538-092-1309

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Patent No. 675314
GENERAL INFORMATION:
APPLICANT: Gloct, Loic
APPLICANT: Gloct, Loic
APPLICANT: Gloct, Loic
APPLICANT: Gloct, Loic
APPLICANT: Gloct, Loic
CURRENT INTEMPRION: Protein-Protein Complexes and Method of Using Same
FILE REPRENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SEQ ID NO 1309
LENGTH: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (0)...(0) OTHER INFORMATION: Polypeptide Accession Number Q13573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: November 10, 2004, 15:57:23 Job time : 7.40214 secs
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280 INENFAKLAEALYIA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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GenCore version 5.1.6
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November 11, 2004, 02:43:24 ; Search time 38.6619 Seconds (without alignments) 146.426 Million cell updates/sec
OM protein - protein search, using sw model
                                                        Run on:
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1 IGEEFSRAAEKLYLAV 16 US-10-092-750-225 76 Perfect score: Scoring table: Sequence:

1568699 seqs, 353819137 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1568699 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

| cgn2 6/ptodata/2/pubpaa/PCT_NEW PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
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| cgn2 6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO0PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO0NBW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 225, App	Sequence 1801, Ap	Sequence 110, App	Sequence 243, App	Sequence 62407, A	Sequence 64714, A	Sequence 53, Appl	Sequence 53, Appl	Sequence 23074, A	Sequence 314, App	Sequence 312, App	Sequence 63869, A	Sequence 6581, Ap
ΙD	US-10-092-750-225	US-09-925-300-1801	US-10-403-571-110	US-09-712-363-243	US-10-282-122A-62407	US-10-282-122A-64714	US-09-880-505-53	US-10-051-643-53	US-10-369-493-23074	US-10-627-476-314	US-10-627-476-312	US-10-282-122A-63869	US-09-738-626-6581
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% Query Match Length DB ID	16	92	428	876	876	876	175	175	186	708	713	886	1111
Query	100.0	81.6	57.9	57.9	57.9	57.9	56.6	56.6	56.6	56.6	56.6	56.6	9.95
Score	92	62	44	44	44	44	43	43	43	43	43	43	43
Result No.	П	7	m	4	Ŋ	9	7	00	თ	10	11	12	13

Sequence 444, App Sequence 61763, A Sequence 61763, A Sequence 61763, A Sequence 61763, A Sequence 6132, A Sequence 6132, A Sequence 6132, A Sequence 6122, A Sequence 6123, A Sequence 61025, A Sequence 61025, A Sequence 61025, A Sequence 1982, A Sequence 1983, A Sequence 111, Appl Sequence 111, Appl Sequence 111, Appl Sequence 11279, A Sequence 112	equence 49573 quence 1285, equence 6501,
US-09-925-302-44 US-09-925-302-44 US-10-282-112-8- US-10-282-122A- US-10-166-225A- US-10-166-225A- US-10-166-225A- US-10-166-225A- US-10-188-626-15 US-10-389-566-11 US-10-41-951-11	US-10-282-122A-4957 US-09-925-300-1285 US-10-369-493-6501
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ALIGNMENTS

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               | Sequence 225, Application US/10092750 |
| Publication No. US20030032157A1 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: Hammond, Philip W. |
| APPLICANT: Alpin, Julia |
| APPLICANT: Wright, Martin C. |
| TITLE OF INVERTION: Polypeptides Interactive with BCL-X1 |
| FILE REFERENCE: 50036/050002 |
| CURRENT APPLICATION WUMBER: US/10/092,750 |
| PRIOR PELILOR DATE: 2001-03-08 |
| PRIOR FILLING DATE: 2001-03-08 |
| PRIOR FILLING DATE: 2001-03-08 |
| NUMBER OF SEQ ID NOS: 253 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 225 |
| LENGTH: 16 |
| TYPE: PRT |
| CRAMISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0;
US-10-092-750-225
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1 iGEEFSRAAEKLYLAV 16

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1 IGEEFSRAAEKLYLAV 16

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Gaps

US-09-925-300-1801 Sequence 1801, Application US/09925300 ; Patent No. US20020151681A1 ; GENERAL INFORMATION:

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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Dyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            631 GYEFSRACESLY 642
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                                                                                                                                                                                                                                                                                                                                           FEATURE:
TWAND KEY: SITE
LOCATION: (777)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (81)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-300-1801
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APPLICANT: Sreve Ruben;
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PALO1
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOCTWARRE: Patentin Ver. 2.0
SEQ ID NO 1801
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.9%; Score 44; DB 15; Length 428; ilarity 56.2%; Pred. No. 42; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 110, Application US/10403571
Sequence 110, Application US/10403571
Publication No. US20040068763A1
GENERAL INFORMATION:
APPLICANT: Hopkins, Nancy
APPLICANT: Golling, Gregory
APPLICANT: Amsterdam, Adam
APPLICANT: Sun, Zhoaxia,
TITLE OF INVENTION: Developmental Mutations in Zebrafish
FILE REFERENCE: 01997/33902.
CURRENT APPLICATION NUMBER: US/10/403,571
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: US 60/368,760
PRIOR PLIING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 159
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO ILENGTH: 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.6%; Score 62; DB 9; Length 92; 100.0%; Pred. No. 0.0059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 9; Conserv
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US-09-712-363-243 ; Sequence 243, Application US/09712363' ; Patent No. US20020164588A1

RESULT 4

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APPLICANT: Rotatein, Sergio H.
APPLICANT: Rotatein, Sergio H.
APPLICANT: Rotatein, Sergio H.
APPLICANT: Rotatein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE APPLICATION NUMBER: D000-11-13
CURRENT FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-02-01
PRIOR PLICATION NUMBER: 60/17,844
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-11-12
PRIOR PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR PLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR PLICATION NUMBER: 60/165,086
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PRIOR PLICATION NUMBER: 60
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APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Prosyth, R.
APPLICANT: Prosyth, R.
APPLICANT: Tu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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US-09-712-363-243
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PRIOR APPLICATION WUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 64714
LENGTH: 876
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Best Local Similarity 75.0
Matches 9; Conservative
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US-10-051-643-53
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TITLE OF INVEXTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-02-02
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-12-22
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PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-24
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR SPEING DATE: 2001-02-16
SCOFTWARE PRIOR APPLICATION NUMBER: 95 SEQ ID NOS: 78614
SOFTWARE PATENTING DATE: 2001-02-16
SOFTWARE PATENTING VERSION 3.1
LENGTH: 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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; Sequence 64714, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeslbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Mycobacterium bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind, Judith
Wall, Daniel
Trawick, John
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            631 GYEFSRACESLY 642
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Best Local Similarity 75.0
Matches 9; Conservative
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Sequence 312, Application US/10627476

Sequence 312, Application US/10627476

Sequence 312, Application US/10627476

Sequence 312, Application US/20040030116A1

Septication No. US20040030116A1

APPLICANT: Pompejus, Mark

APPLICANT: Schoder, Hartwid

APPLICANT: Schoder, Josephaner, Gregor

TITLE OF INVENTION: TRANSPORT

FILE OF INVENTION WUMBER: US/80/602/78

PRIOR PAPLICATION WUMBER: DB 19931454.3

PRIOR APPLICATION WUMBER: DB 1993122.1

PRIOR PLILNG DATE: 1999-07-08

PRIOR PLILNG DATE: 1999-07-08

PRIOR PLILNG DATE: 1999-07-08

PRIOR PLILNG DATE: 1999-07-08

PRIOR PLILNG DATE: 1999-07-09

PRIOR PLILNG DATE: 1999-07-09

PRIOR APPLICATION WUMBER: DB 19931128.0

PRIOR PLILNG DATE: 1999-07-09

PRIOR PLILNG DATE: 1999-0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932180.9
PRIOR PILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 678
LENGTH: 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 56.6%; Score 43; DB 15; Length 708; Best Local Similarity 53.3%; Pred. No. 1.1e+02; Matches 8; Conservative 3; Mismatches 4: Indela
                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-627-476-314
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APPLICANT: Slater, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FURENT PAPLICATION NUMBER: US/10/369,493
CURRENT PAPLICATION NUMBER: US 6/360,039
PRIOR PLILING DATE: 2002-02-21
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Sequence 314, Application US/10627476

Publication No. US20040030116A1

Sequence 314, Application Wo. US20040030116A1

Sequence 314, Application No. US20040030116A1

APPLICANT: Schoder, Hartwig

APPLICANT: Schoder, Hartwig

APPLICANT: Schoder, Burkhard

APPLICANT: Bearlauer, Gregor

TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE

TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE

TITLE OF INVENTION: INVOLVED IN MEMBRANE

TITLE OF INVENTION: TANSPORT

TITLE OF INVENTION: TANSPORT

TITLE OF INVENTION NUMBER: US/602,787

PRIOR FILING DATE: 1099-06-25

PRIOR FILING DATE: 1999-07-08

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Pred. No. 25;
2; Mismatches 3; Indels
                                                                               Score 43; DB 13; Length 175;
Pred. No. 24;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23074, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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Best Local Similarity 61.5%;
Matches 8; Conservative 3
                                                                                   Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
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US-10-369-493-23074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23074
LENGTH: 186
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62 GEDFSRKTEKEYI 74
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US-10-369-493-23074
                  US-10-051-643-53
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Gaps
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Query Match 56.6%; Score 43; DB 15; Length 713; Best Local Similarity 53.3%; Pred. No. 1.1e+02; Matches 8; Conservative 3; Mismatches 4; Indels
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Sequence 444, Application US/09925302
| Patent No. US2020044941A1
| Patent No. US2020044941A1
| Patent No. US2020044941A1
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAIG4
| CURRENT APPLICATION NUMBER: US/09/925,302
| CURRENT FILING DATE: 2001-08-10
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 896
| SOFTMARE: PatentIN Ver. 2.0
| SEQ ID NO 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1111;
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; Sequence 444, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
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56.6%; Score 43; DB 9; 3
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 3; Mismatches 4
                                                                                       APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
ITILE DO INTENTION: NOVEL POLYNUCLEOTIDES
ITILE REPERBNCE: 249-125
CURRENT FILING DATE: 2000-12-18
FRICA APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRICA APPLICATION NUMBER: UP 99/377484
PRICA APPLICATION NUMBER: UP 00/159162
PRICA APPLICATION NUMBER: UP 00/159162
PRICA APPLICATION NUMBER: UP 00/260988
PRICA FILING DATE: 2000-04-07
PRICA FILING DATE: 2000-08-03
PRICA FILING DATE: 2000-08-03
SOFTWARE: PARENTIN VOY: 3.0
SEQ ID NO 6581
LENGTH. 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6581
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763 VSEEIAREVEKLFLA 777
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          YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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US-09-925-302-444
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFRENCE: ELITRA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PELICATION NUMBER: 60/202,727

PRIOR PELING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/203,347

PRIOR PILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-10-29

PRIOR PLING DATE: 2000-10-29

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-29

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2000-02-16

PRIOR PLING DATE: 2000-03-16

PRIOR PLING DATE: 2000-03
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                                                                                                                                                                                             Sequence 63869, Application US/10282122A
PUBLICATION NO. US20046029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Oyskind, Judith
APPLICANT: Tyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Panamoto, Robert
APPLICANT: POTSYTH, R.
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US-09-738-626-6581
US-09-738-626-6581, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NARAGAMA, SATOSHI
APPLICANT: NIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Mycobacterium leprae US-10-282-122A-63869
: || :| || || || 365 VSEEIAREVEKLFLA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641 GYEFSRACEALY 652
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                                                                                                        RESULT 12
US-10-282-122A-63869
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Best Local Similarity 53.3%; Pred. No. 68;
Matches 8; Conservative 3; Mismatches 4; Indels
; PRIOR APPLICATION NUMBER: PCT/US00/05918; PRIOR FILING DATE: 2000-03-08; PRIOR APPLICATION NUMBER: 60/124,270; PRIOR RILING DATE: 1999-03-12; PRIOR FILING DATE: 1999-03-12; SCTWARE: Patentin Ver: 2.0; SEQ ID NO 444; LENGTH: 323; TYPE: PRT: ORGANISM: Homo sapiens US-05-925-302-444
                                                                                                                                                                                                                                                                                                                                                       1 IGEEFSRAAEKLYLA 15
| | | :: | | | :|
283 INENFAKLAEALYIA 297
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Search completed: November 11, 2004, 07:41:47 Job time : 39.6619 secs

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November 10, 2004, 14:52:32; Search time 5.46619 Seconds (without alignments)
281.634 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                       OM protein - protein search, using sw model
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BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-092-750-225 76 1 IGEEFSRAAEKLYLAV 16 Title: Perfect score: Sequence: Scoring table:

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* 2: pir1:* 3: pir2:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	ignal rec	gnal	signal recognition	_	cyclin A2 - Africa	probable valS prot	mitotic-specific c	shikimate kinase (puff-specific nucl	valyl-tRNA synthas	hypothetical prote	probable transcrip	- Africa	iron-dependent rep	transcription regu	probable cyclin, 2	ica	related to sorbito	conserved hypothet	hypothetical prote	mitosis-specific c	lysk family regula	ical	cycli	mito		cal	cal prot	ein
		7292	4	\sim	N	151637	0	m	9	56	87	32	83	S11678	694	B97313	H96512	T19538	T51897	H69162	S76464	871193	AE1019	7164	628	9680	4103	4076	8306	517
	h DB					2																								
	Length	8	œ	œ	40	415	87	S	18	54	88	24	30	41	19	31	32	34	34	34	46	22	29	44	45	45	88	7	σ	13
ako (Query		н	н	~	57.9	^	9	9	9	9	ß	S	Ŋ	m	m	3	3	m	3	n	2	N	N	2	S	S	\vdash	4	н
	Score					44			43	43	43	42	42	42	41	41	41	41	41	41	41	40	40	40	40	40	40	39	<u>გ</u>	e M
`	Result No.		7	m	4	5	y	7	€	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Gaps

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EEFSRAAEKLYLA 15

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probable transposa regulator of pssA	Lysk-family transc	probable transcrip	transcription regu	probable electron	transcription regu	conserved hypothet	cyclin A - chicken	cyclin A - bovine	cyclin A - mouse	cyclin A2 - mouse	cyclin A - human	Similar to Cytochr	hypothetical prote	hypothetical prote
G95912 B91216	AF0475	B83416	C82387	D72768	875062	AB0435	838812	\$24788	S37280	S38501	S08277	D86306	T25379	H72422
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195	293	301	306	308	316	328	395	406	422	422	432	476	535	539
51.3	51.3	51.3	51.3	51.3	51.3	51.3	51.3	51.3	51,3	51.3	51.3	51.3	51.3	51.3
6 6 6 6	36	39	39	33	39	39	39	39	33	39	39	33	39	ტ ტ
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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signal recognition particle 9K chain - dog
Cispecies: Camis lupus familiaris (dog)
Cipate: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
CiAccession: A34731
RiStrub, K.; Walter, P.
And. Cell. Biol. 10, 777-784, 1990
A;Title: Assembly of the Alu domain of the signal recognition particle (SRP): dimerization A;Reference number: A34731; MUID:90136594; PMID:2153922
                                                                                                                                                                                                                       A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-86 cHSU>
A/Residues: 1-86 cHSU>
A/Cross-references: UNIPROT:P49458; GB:U20998; NID:g897850; PIDN:AAA70170.1; PID:g897851
A/Note: authors translated the codon CCG for residue 2 as Ala, and GAG for residue 86 as C/Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: A34731
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-86 <STR>
A,Cross-references: UNIPROT:P21262, GB:M34952; NID:g164085; PIDN:AAA30897.1; PID:g164086
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81.6%; Score 62; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

81.6%; Score 62; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: GDB:SRP9
A,Cross-references: GDB:128862; OMIM:600707
A,Map position: 5q21-5q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 EEFSRAAEKLYLA 15
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A34731
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Gaps

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Cipecies: Mycobacterium tuberculosis (strain H37kV)
Cipecies: Mycobacterium tuberculosis
Cipate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
CiAccession: G70863
RicOle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davises, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atthers Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Recession: G70863
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DAA,
A; Accession: Lype: DAA,
A; Lype A;Molecule type: DAA,
A; Lype A; Lype A; Lype A;
A; Lype A; Lype A;
A; Lype A; Lype A;
A; Lype A; Lype A;
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A;Residues: 1-56 <82A>
A;Cross-references: UNIPROT:039327; EMBL:L25402
A;Note: the sequence of residues 1-2, 51-56 and the corresponding nucleic acid sequence c)
G;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reders 1-870-5 COL>
A;Rederses 1-87 Colosa references: UNIPROT:053175; GB:AL021246; GB:AL123456; NID:G3261507; PIDN:CAA1602!
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: 553000 2.3 Schaerer, S.; Moloney, M. Plant, S.; Fitch, M.; Schaerer, S.; Moloney, M. Plant Mol. 27, 263-275, 1995 A;Title: Classification and expression of a family of cyclin gene homologues in Brassica A;Title: Classification and expression of a family of cyclin gene homologues in Brassica A;Teference number: 552996; MUID:95195155; PMID:7888617 A;Accession: 553000 A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitotic-specific cyclin CYC2.3 - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 21-Apr-1997 #sequence_revision 21-Apr-1997 #text_change 12-Jul-2004
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0
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                                                                                                                                 Query Match
57.9%; Score 44; DB 2; Length 415;
Best Local Similarity 56.2%; Pred. No. 7.2;
Matches 9; Conservative 2; Mismatches 5; Indels
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Pred. No. 16;
0; Mismatches 3; Indels
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C;Keywords: cell cycle control; cell division; mitosis
C;Superfamily: cyclin, A/B/D/E type C;Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                 203 VGEEYKLQNETLYLAV 218
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A,Gene: valS
C,Superfamily: valine-tRNA ligase
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Best Local Similarity 75.0%;
Matches 9; Conservative (
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C; Superfamilw:
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A; Description: The 9kD subunit of the murine signal recognition particle.
A; Reference number: S57500
A; Accession: S57500
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-86 < BUI>
A; Residues: 1-86 < BUI>
A; Cross-references: UNIPROT: P49962; EMBL: X78304; NID: G872130; PIDN: CAA55114.1; PID: G8721
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DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyn
A;Reference number: A72450; MUID:99310339; PMID:10382966
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Experimental source: strain K1;
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CySpecies: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Daces: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 12-Jul-2004
C;Accession: 151637; S52713
R;Howe, J.A.; Howell, M.; Hunt, T.; Newport, J.W.
Genes Dev. 9, 1164-1176, 1995
R;Howe, J.A.; Howell, M.; Hunt, T.; Newport, J.W.
A;Rible: Identification of a developmental timer regulating the stability of embryonic A;Reference number: 151637; MUID:95278730; PMID:7758942
A;Accession: 151637
A;Molecule type: mRNA
A;Residues: 1-415 <HOW>
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B72778
                                                                                                                                                                                                                   signal recognition particle - mouse
C.Species: Mus musculus (house mouse)
C.Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C.Accession: S57500
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C;Superfamily: mitochondrial processing peptidase alpha chain
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93 VSDSLARVAEKLFLAV 108
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              8 EEFSRAAEKLYLA 20
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A; Residues: 1-403 < KAW>
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A; Status: preliminary
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Valy1-tRNA synthase [imported] - Mycobacterium leprae
Valy1-tRNA synthase [imported] - Mycobacterium leprae
Valy1-tRNA synthase [imported] - Mycobacterium leprae
C;Species: Wycobacterium leprae
C;Species: Wycobacterium leprae
C;Species: Wycobacterium leprae
C;Accession: A87031
R; Davies, R.M.; Davin, R.; Duthoy, S.; Feltwell, T.; Fraser, A.; Wheeler, P.R.; Hor R; Davies, R.M.; Mtherford, K.M.
M.A; Rutherford, K.M.
Mature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sqn
A;Reference number: A86909; MulD:21128732; PMID:11234002
A;Reference number: A86909; MulD:21128732; PMID:11234002
A;Reference DNA
A;Reference DNA
A;Reference NA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT:Q9CBY7; GB:AL450380; NID:g13093326; PIDN:CAC30422.1; GSPDB:GR
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         Length 547;
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A)Description: The sequence of C. elegans cosmid F59E11
A;Reference number: 221124
A;Accession: T32122
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A,Molecule type: DNA
Score 43; DB 2;
Pred. No. 15;
4; Mismatches
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Pred. No. 9.3;
2; Mismatches
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Pred. No.
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A;Introns: 87/3; 123/3; 180/3; 217/3
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75.0%;
         53.3%;
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C,Superfamily: valine-tRNA ligase
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Best Local Similarity 66.7%;
Matches 8; Conservative
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152 KEFSECAEKLYV 163
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                                                                                                  8; Conservative
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         Query Match
Best Local Similarity
Matches 8; Conserv
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A;Gene: CESP:F59E11.5
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Matches
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                                                                         shikimate kinase (BC 2.7.1.71) arol - Bacillus subtilis
clipate: solilus subtilis
Clipate: 10.5ep-1999 #text_change 09-Jul-2004
Clipate: 10.5ep-1999 #text_change 09-Jul-2004
Clipate: 10.5ep-1999 #sequence_revision 10.5ep-1999 #text_change 09-Jul-2004
Ribakana, A.; Ogawa, X.; Nakamura, X.; Yamane, K.
J. Ferment. Bioeng: 77, 312-314, 1994
A;fitler Nucleocide sequence of the shikimate kinase gene (arol) of Bacillus subtilis.
A;Accession: 119782
A;Acteror number: 119782
A;Atthors number: 119782
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A;Residues: 1-186 <kUN>
A;Cross-references: GB:Z99105, GB:AL009126, NID:g2632457; PIDN:CAB12109.1; PID:g2632601 A;Experimental source: strain 168
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A56575
puff-specific nuclear protein Bx42 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A56575
R;Waland, C.; Mann, S.; von Besser, H.; Saumweber, H.
Chromosoma 101, 517-525, 1992
A;Title: The Drosophila nuclear protein Bx42, which is found in many puffs on polytene A;Reference number: A56575; MuID:93048378; PMID:1424996
A;Accession: A56575
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A;Residues: 1-547 <WIE>
A;Crossreferences: UMIPROT: P39736; GB:X64536; GB:S48763; NID:g8391; PIDN:CAA45834.1; A;Note: sequence extracted from NCBI backbone (NCBIN:118716, NCBIP:118718) C;Genetics:
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S;Superfamily: shikimate kinase, shikimate kinase homology
C;Keywords: arcmatic amino acid biosynthesis; ATP; magnesium; phosphotransferase
P;10-124/Domain: shikimate kinase homology <SKI>
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A;Cross-references: FlyBase:FBgn0004856
C;Superfamily: Caenorhabditis elegans hypothetical protein T27F2.1
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Pred. No. 4.7;
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Best Local Similarity 61.5
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEEFSRAAEKLYL 14
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transcription regulator, LysR family [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: B97313 R;Nolling, U; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. Bennett, G.N.; Koonin, E.V.; Smith, D.R. A;Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clost A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Cross-references: UNIPROT:028489; GB:AE000979; GB:AE000782; NID:g2689302; PIDN:AAB89462
C;Superfamily: conserved hypothetical protein MJ0568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q97DV9; GB:AE001437; PIDN:AAK81293.1; PID:g15026445; GSPDB:G3
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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Pred. No. 18;
3; Mismatches 2; Indels
                                                                                                   Query Match 53.9%; Score 41; DB 1; Length 191; Best Local Similarity 53.3%; Pred. No. 11; Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: November 10, 2004, 15:55:08 Job time : 5.46619 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.9%;
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                            2 GEEFSRAAEKLYLAV 16
                                                                                                                                                                                                                                                                                   65 GEELARRIKKYYLAL 79
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-312 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Gene: CAC3361
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                                                                                                                                  Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathology A; Reference number: A82950; MJID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-302 <STO>
A;Cross-references: UNIPROT:09HXL9; GB:AE004796; GB:AE004091; NID:g9949939; PIDN:AAG0716
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P18606; EMBL:X53745; NID:g64644; PIDN:CAA37775.1; PID:g64645
C;Superfamily: cyclin, A/B/D/E type
C;Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Minshull, J.; Golsteyn, R.; Hill, C.S.; Hunt, T.
EMBO J. 9, 2865-2875, 1950
A;Title: The A- and B-type cyclin associated cdc2 kinases in Xenopus turn on and off at AxEference number: S11678; WUID:90360999; PMID:2143983
A;Accession: S11678
          probable transcription regulator PA3776 [imported] - Pseudomonas aeruginosa (strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                             C;Specides: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cyclin A - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 12-Jul-2004
C;Accession: S11679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 12;
3; Mismatches 0; Indels
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Gene: PA3776 superfamily: Pseudomonas putida regulatory protein catR

C; Genetics:

A;Status: preliminary A;Molecule type: DNA A; Accession: F83174

55.3%;

Query Match Best Local Similarity

Best Loc Matches

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RESULT 13 S11678

8; Conservative 5 FSRAAEKLYLA 15 19 FSRAAERLFVA 29 Tron-dependent repressor homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: H69472
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F. Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Atle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaech number: A69250; MUID:98049343; PMID:9389475

A;Accession: H69472
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-191 <KLE>

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Gaps

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DB 2; Length 418; 17; 5; Indels

3; Mismatches

Query Match 55.3%; Score 42; Best Local Similarity 50.0%; Pred. No. 1 Matches 8; Conservative 3; Mismatch

A; Molecule type: mRNA A; Residues: 1-418 <MIN>

207 VGEEYKLHTETLYLAM 222

1 IGEEFSRAAEKLYLAV 16

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 10, 2004, 14:50:40; Search time 26.8185 Seconds (without alignments) 343.270 Million cell updates/sec Run on:

US-10-092-750-225 76 1 IGEEFSRAAEKLYLAV 16 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q6p2s0 homo sapien	1 hom	Q6nvx0 homo sapien	Q8wtw0 homo sapien	15 hon	P21262 canis famil	P49458 homo sapien		Aah66957 homo sapi	Bac34557 mus muscu		Q8iy91 homo sapien			~	gloe			_	æ			Q9pw43 carassius a		brachydani	2 br	3 brachy	P47827 xenopus lae	xenobns		Q9i8j1 carassius a
SUMMARIES		qi	28	AAH64351	QENIVXO	QSWTWO	AAH67845	SR09_CANFA	SR09_HUMAN	SR09_MOUSE	AAH66957	BAC34557	Q7ZW94	QBIY91	CGA1 HUMAN	Q7T3L6	086323	Q7NG14	CGA1 MOUSE	QBC5U1	Q765S2	4	CGA1_CARAU	Q9PW42	Q9PW43	Q9YFN7	Q6NV43	Q72VJ2	AAH68323	CGA2_XENLA	Q6DE80	берінв	0918J1
		DB	N	N	Ŋ	N	7	Н					7	7	Н	(1	7	0	п	7	0	N	ч	α	7	7	0	7	(1	Н	7	71	0
		Match Length	49	49	82	82	82	85	85	85	86	86	86	464	465	390	395	301	421	421	270	270	391	391	391	403	410	410	410	415	415	415	428
	* Ouerv	Match			81.6		81.6									63.2																	
		Score	62	62	62	62	62	62	62	62	62	62	52	20	50	48	48	47	46	46	44	44	44	44	44	44	44	44	44	44	44	44	44
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Q98ta3 brachydanio O8i2z0 methanococc	£3016				Q8xhml clostridium	Q7vv47 bordetella		Q7q9y9 anopheles g	Q9rdjl streptomyce	Q9vdd0 drosophila	Aag23542 drosophil	P39736 drosophila
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Q98TA3	CAF30163	SYV_MYCTU	039327	AROK BACSU	Q8XHM1	Q7VV47	Q92JX0	Q7Q9Y9	Q9RDJ1	O3VDD0	AAQ23542	BX42_DROME
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428	236	876	57	186	289	301	307	329	344	393	393	547
57.9	57.9	57.9	56.6	9.95	9.95	56.6	56.6	56.6	9.95	56.6	56.6	56.6
4.4	1. 4. 1. 4.	44	43	43	43	43	43	43	43	43	43	43
32	3 5	35	36	37	38	39	04	41	42	43	44	45

ALIGNMENTS

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InterPro; IPR008832; SRP9.
InterPro; IPR009018; SRP9/14.
Pfam, PP05486; SRP9; 1.
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                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRP9 protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                 Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.6%; Score 62; DB 2; Length 49; 100.0%; Pred. No. 0.0036; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB=Brain;
MEDIINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4351; AAH64351.1; -.
49 AA; 5769 MW; 3E90E32103B227DF CRC64;
                                               02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 AA.
                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.'
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
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                         PRELIMINARY;
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                                                                                        SRP9 protein.
Homo sapiens (Human)
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                                                                                                                                            NCBI_TaxID=9606;
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Name=SRP9;
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                          AAH64351
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QENVXO
RESULT 2
            AAH64351
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RC TISSUE=Bone marrow,

RX MEDINE=2238257; PubMed=12477932;

RX Atausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

RA Attausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hsieh F.,

RA Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Morlan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,

RA Richards S.M., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Hilalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,

RA Hilling M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Hiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Altakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Richards S.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Torywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length human
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A hischis F.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C., Rah S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzney K.J., Males J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Garen B.D., Dickson M.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S., Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 0.006;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitred (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC067845; AAH67845.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 AA; 9124 MW; D4C817FE1A6D7ED5 CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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us-10-092-750-225.rup

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Gaps

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Pred. No. 0.006; ; Mismatches 0; Indels

100.08;

Best Local Similarity 100. Matches 13; Conservative 3 EEFSRAAEKLYLA 15

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TISSUB-Brain;

WEDLINE=22388257; PubMed=12477932;

RETARUSPERS R.L.; Feingold E.A., Grouse L.H., Derge J.G.,

RETARUSPERS R.L.; Feingold E.A., Grouse L.H., Derge J.G.,

RIJUSHOR R.L.; Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Joedan H., Moore T., Max S.L., Mang J., Haste F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninol E.M., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robers S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Helton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

M. Jones S.J., Marra M.A.;

R and mouse CDNA sequences.",

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                              Straubberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC021995; AAH21995.1; -.
HSSP; P49488; IEBO.
GO; GO:0005786; C:signal recognition particle; IEA.
GO; GO:000373; F:RNA binding; IEA.
GO; GO:0045900; P:negative regulation of translational elonga...
GO; GO:0046900; P:negative regulation of translational elonga...
InterPro; IPR008032; SRP9.
InterPro; IPR009018; SRP9/14.
SEQUENCE 82 AA; 9142 MW; D4C81093DA6D7ED5 CRC64;
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81.6%; Score 62; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels
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D4C817FE1A6D7EDS CRC64;
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-APR-2004 (TrEMBLrel. 27, 14-APR-2004 (TrEMBLrel. 27, 14-APR-2004 (TrEMBLrel. 27,
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SEQUENCE FROM N.A.
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81.6%; Score 62; DB 2; Length 82;

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REPLINE=90136594; PubMed=2153922;
REPLINE=90136594; PubMed=2153922;
REPLINE=90136594; PubMed=2153922;
REPLINE K., Walter P.;
RT dimerization of the Alu domain of the signal recognition particle (SRP):
dimerization of the two protein components is required for efficient
RT dimerization of the two protein components is required for efficient
RT dimerization of the two protein components is required for efficient
RT dimerization of the two protein components is required for efficient
RT dimerization of the RNA.";
LI FUNCTION: Signal-recognition-particle assembly has a crucial role
cof SRP together with SRP14 and the Alu portion of the SRP
RNA, constitutes the elongation arrest domain of SRP. The complex
COF SRPP and SRP14 is required for SRP RNA binding.
COF SUBGNIT: Signal recognition particle consists of a 7S RNA molecule
of 300 nucleotides and six protein subunits: SRP72, SRP68, SRP54,
COF SUBCELLULAR LOCATION: Cytoplasmic.
COF SIMILARITY: Belongs to the SRP9 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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InterPro; IPR008832; SRP9.
InterPro; IPR009018; SRP9/14.
Pfam; PF05486; SRP9; 1.
Direct protein sequencing; RNA-binding; Signal recognition particle.
INIT MET 0
                                                                                                                                      Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 AA; 9914 MW; 047EA875B270B450 CRC64;
                                      01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Signal recognition particle 9 KDa protein (SRP9).
Name-SRP9;
85 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 33, Created)
(Rel. 33, Last sequence update)
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  STANDARD;
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ID SR09 HUMAN
AC P49458;
DT 01-FEB-1996 (I
  CANFA
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Pfam; PF05486; SRP9; 1
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MEDINES-2288257; PubMed=12477922; DOI=10.1073/pnas.242603899;

MITAGESER R.D., Feligold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wand J., Hisleh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Sheilus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Medicus A., Schein J.E., Jones S.J.M., Marra M.A.,

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                                                                                                                                                                                                                                               Hsu K., Chang D.-Y., Maraia R.J.; "Human signal recognition particle (SRP) Alu-associated protein also binds Alu interspersed repeat sequence RNAs. Characterization of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              In targeting secretory proteins to the rough endoplasmic reticulum membrane. SRP9 together with SRP14 and the Alu portion of the SRP RNA, constitutes the elongation arrest domain of SRP. The complex of SRP9 and SRP14 is required for SRP RNA binding.

-I-SUBUNT: Signal recognition particle consists of a 7. SNA molecule of 300 nucleotides and six protein subunits: SRP72, SRP68, SRP54, SRP19, SRP14 and SRP9.
-I-SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM, 600707; -. Gisignal recognition particle receptor complex; TAS. GO; GO:0005785; C:signal recognition particle receptor complex; TAS. GO; GO:0005047; F:signal recognition particle binding; TAS. InterPro; IPR008932; SRP9. InterPro; IPR009018; SRP9/14.
                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                     Signal recognition particle 9 kDa protein (SRP9).
Name=SRP9;
  01-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 270:10179-10186(1995).
                                                                                                                                                                                                                          AEDLINE=95247726; PubMed=7730321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U20998; AAA70170.1; -.
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PDB; 1E80; X-ray; A/C=1-85.
PDB; 1E8S; X-ray; A=1-85.
IntAct; P49458; -.
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Genew; HGNC:11304; SRP9.
                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                  WCBI_TaxID=9606;
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REP SECUENCE FROW N.A.

REPAINCECTEL/GAIL TISSUE=Embryo, and Urinary bladder;

REALINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA OKAZAKI Y.; Furuno M., Kasukawa T., Adachi J., Bono H.; Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Samanaka I., Kiyosawa H.,

RA Mikaido I., Osato N., Saito R., Suzuki H., Samanaka I., Kiyosawa H.,

RA Mikaido I., Osato N., Bult C., Hume D.A., Quackenbush J.,

RA Balake J.A., Bradt D., Bult C., Hume D.A., Quackenbush J.,

RA Blake J.A., Bradt D., Bult C., Hume D.A., Quackenbush J.,

RA Blake J.A., Bradt D., Bult C., Hume D.A., Quackenbush J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., King B.L.,

RA Anai A., Kawaju H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Anai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Retrovsky N., Pillai R., Pontius J.U., Qil D., Ramachandram S.,

Sultana R., Takenska Y., Taylor M.S., Teasdala R.D., Tomita M.,

Sultana R., Takenska Y., Taylor M.S., Teasdala R.D., Tomita M.,

Nurando L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

Yuan Z., Zavolam M., Zhu Y., Zimmer A., Carninci P., Hayatsu M.,

Hincane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
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MEDLINE=94301784; PubMed=7518078;
BOVIA F., Bui N., Strub K.;
"The heterodimeric subunit SRP9/14 of the signal recognition particle functions as permuted single polypeptide chain.";
Nucleic Acids Res. 22:2028-2035(1994).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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RNA-binding; Signal recognition particle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9980 MW; BFB1E9ECAF70A0E4 CRC64;
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P49962; Q9D085;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Signal recognition particle 9 kDa protein (SRP9).
                                       By similarity.
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Best Local Similarity 1vv...
Best Local Similarity 1vv...
- And 13; Conservative
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3D-structure; FINIT MET
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REQUENCE FROW NA.

RECURSINE R.D., Collins F.A., Grouse L.H., Derge J.G.,

RIAUSNER R.D., Collins F.A., Grouse L.H., Derge J.G.,

RAIschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Bactow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Bactow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Dokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Hownstein M.J., Usdin T.B., Poshiyuki S., Carninci P., Prange C.,

RA Bras S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Hilalon D.K., Muxny D.M., Sodergran B.J., Lu X., Gibbs R.A.,

RA Hilalon D.K., Muxny D.M., Sodergran B.J., Lu X., Gibbs R.A.,

RA Hatcheld N., Schorlen B.J., Carbina S., Sanchez A.,

RA Hatcheld Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A. Schehn J.B., Jones S.J.M., Marra M.A.;

RA Goderstion and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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X-RAY CRYSTALLOGRAPHY (2.53 ANGSTROMS) IN COMPLEX WITH SRP14.

IN MEDLINE-97377014; PubMed=9233785;

Birse D.E., Kapp U., Strub K., Cusack S., Aaberg A.;

Dinding heterodiner, SRP9/14.";

EMBO J. 16.3757-3766(1997).

IL FUNCTION: Signal-recognition-particle assembly has a crucial role in targeting secretory proteins to the rough endoplasmic reticulum membrane. SRP9 together with SRP4 and the Alu portion of the SRP RNA, constitutues the elongation arrest domain of SRP. The complex of SRP9 and SRP4 is required for SRP RNA binding.

C.: SUBUNIT: Signal recognition particle consists of a 7S RNA molecule of 300 nucleotides and six protein subunits: SRP72, SRP68, SRP54, SRP19, SRP14 and SRP9.

C.: SUBCELLULAR LOCATION: Cytoplasmic.
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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EMEL, X78304; CAA55114.1; -..

EMEL, AK01720; BA27800.1; -..

EMEL, AK020620; BA32138.1; -..

EMEL, BC039648; AAH39648.1; -..

EMEL; BC039648; AAH39648.1; -..

EMEL; BC039648; AAH39648.1; -..

EMEL; BC039648; AAH39648.1; -..

MCD; MG1:1350930; SRP9.

InterPro; IRR008932; SRP9.

InterPro; IRR00918; SRP9/14.

Pfam; PF05486; SRP9; 1...

EMER; BC5486; SRP9; 1...

EMEL; BC5486; SRP9; 1...

EMER; BC5486; SRP9; 23 23 31 31 21 21 25 25 HELIX TURN STRAND

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MEDINE-223825;

MEDINE-223825;

MEDINE-223825;

MEDINE-223825;

MEDINE-223825;

MEDINE-223825;

MEDINE-223825;

MALSCHIE R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

RA Broachenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

RA Raba S.S., Loquellano N.A., Peers G.J., Abramon R.D., Mullahy S.J.,

RA Raba S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M. K., Gibbs R.A.,

Villalon D.K., Muzny D.W., Sodergren B.D., Lu X., Gibbs R.A.,

RA Fabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Richards S. C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R Topeneration and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                  81.6%; Score 62; DB 1; Length 85; 100.0%; Pred. No. 0.0063; ive 0; Mismatches 0; Indels
32 35
47 52
54 54
55 57
85 A3, 10063 MW; 01C529D4714C62AD CRC64;
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AAH66957;
03-WAR-2004 (TrEMBLrel. 27, Created)
03-WAR-2004 (TrEMBLrel. 27, Last sequence update)
03-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Signal recognition particle 9kDa.
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Best Local Similarity 100.
Matches 13; Conservative
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SEQUENCE
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Score 62; DB 2; Length 86; Pred. No. 0.0063; 0; Indels 100.0%; Pred. 81.6%; 13; Conservative Similarity Query Match Best Local

TISSUE=Brain;
Strausberg R.;
Strausberg R.;
Submitred (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC066957; AAH66957.11; -.
SEQUENCE 86 AA; 10112 MW; DB2CA071AF0E6F65 CRC64;

and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

SEQUENCE FROM N.A.

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3 BEFSRAABKLYLA 15 B EEFSRAAEKLYLA 20

8

RESULT 10 BAC34557

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EMBL; AKO51208; BAC34557.1; -. SEQUENCE 86 AA; 10194 MW; 655860497132AD2C CRC64;
                                                                                         Query Match
Best Local Similarity 100."
Matches 13, Conservative
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EEFARAEKLYL 19
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Matches 11; Conserv
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                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUB=Spinal ganglion; MBDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Nuramatsu M., Hayashizaki Y., Itoh M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayasahida K., Hayasahida K., Hayasahida K., Hayasahida K., Hayasahida K., Hayasahida K., Ishini Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakarume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Thagami T., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                            14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DI30016J12 product:signal recognition particle 9 kDa, full insert sequence.
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MEDLINE=C57BL/61 TISSUE=Spinal ganglion;
MEDLINE=C57BL/62 FubMed=11076861;
MEDLINE=C57BL/62 FubMed=11076861;
MEDLINE=C57BL/62 FubMed=11076861;
MEDLINE=C57BL/62 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=1107 FubMed=110
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CSTBL/66; TISSUE=Spinal ganglion;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
   86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
STRAIN=CS7BL/61, TISSUE=Spinal ganglion,
MEDLINE=22154683; PubMed=12466851;
The FANTOM CONSOTTIUM,
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STRAIN=C57BL/6J; TISSUE-Spinal ganglion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=Spinal ganglion;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
PRELIMINARY;
                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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RECTISSUE=Monle body;

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GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0045900; P:negative regulation of translational elonga. .; IEA.
GO; GO:0006605; P:protein targeting; IEA.
InterPro; IRRO9812; SRP9.
InterPro; IRRO99018; SRP9/14.
Pfam; PF05486; SRP9;
                                                                                                                           Gaps
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01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Name-zgc:5668,
Name-zgc:5668,
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Cyprinidae; Danio.
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81.6%; Score 62; DB 2; Length 86; 100.0%; Pred. No. 0.0063; ive 0; Mismatches 0; Indels
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TISSUE=Whole body;
Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BO049522; AAH49522.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10076 MW; 6E853A3ABA7FAF33 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.-!- SIMILARITY: Belongs to the cyclin family.
EMBL; BC036346; AAH36346.1; -- HSSP; P20248; IFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART, SM00385, CYCLIN; 2.
PROSITE, PS00292; CYCLINS; 1.
Cell cycle; Cell division; Cyclin.
SEOUENCE 464 AA; 52229 MW; E67C6E6D741B7D73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005534; Cinucleus; IEA.
GO; GO:0005534; Cinucleus; IEA.
GO; GO:000074; P:regulation of cell cycle; IEA.
InterPro; IPR00457; Cyclin.
InterPro; IPR011028; Cyclin.
InterPro; IPR06671; Cyclin.
InterPro; IPR06671; Cyclin.
Pfam; PF02884; Cyclin.
Pfam; PF00134; Cyclin.
Pfam; PF00134; Cyclin.
Fig. 1.
                                                                464 AA
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                                                                                               Created)
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                                                                                           01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 62.5
Matches 10, Conservative
                                                              PRELIMINARY;
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                                                                                                                                                                                                                                NCBI_TaxID=9606;
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CGA1_HUMAN
ID CGA1_HUMAN
AC P78396;
                                                                                                                                                 Cyclin A1.
Name=CCNA1;
                                                            OBIY91
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Q8IY91
                                                                ALD DAY BEEN AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND DEAR BY AND D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBDNIT: Interacts with the CDK2 and the CDC2 protein kinases to form a serine/threonine kinase holoenzyme complex. The cyclin subunit imparts substrate specificity to the complex. Does not bind CDK4 and CDK5 (in virro). The cyclin Al-CDK2 complex interacts with transcription factor E2F-1 and RB proteins.
-!- TISSUE SPECIFICITY: Very high levels in testis and very low levels in DEVELOPMENTAL STAGE: Expression increases in early G1 phase and reaches highest levels during the S and G2/M phases.
-!- SIMILARITY: Belongs to the cyclin family. Cyclin AB subfamily.
                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Myeloid;
MEDLINE=97193609; PubMed=9041194;
Yang R., Morosetti R., Koeffler H.P.;
"Characterization of a second human cyclin A that is highly expressed in testis and in several lenkemic cell lines.";
Cancer Res. 57:913-920(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Testis;
Perkins E.L., Wood V.J., Sterling J.F., Hashem V.I., Resnick M.A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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GO; GO:0005829; Cr:cytosol; TAS.

RG; GO:0000741; Primale meiosis I; TAS.

RG; GO:0000743; Priegulation of cell cycle; TAS.

RG; GO:0007239; Priegulation of cell cycle; TAS.

RG; GO:0007239; Priegulation of cell cycle; TAS.

R InterPro; IPR004367; Cyclin_Cterm.

R InterPro; IPR006671; Cyclin_Ike.

R Pfam; PF00134; Cyclin_C; 1.

R Pfam; PF00134; Cyclin_S; 1.

R Pfam; PF00134; Cyclin, Meiosis; Mitosis.

Cell Cycle; Cell division; Cyclin; Meiosis; Mitosis.

CDOMAIN.

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C9C023EEA1CF036D CRC64;
Created)
Last sequence update)
Last annotation update)
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EMBL; U97680; AAB60863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 55-465 FROM N.A.
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Reactome; P78396; -.
30-MAY-2000 (Rel. 39,
30-MAY-2000 (Rel. 39,
05-JUL-2004 (Rel. 44,
                                                                                                Cyclin Al.
Name=CCNAl;
Homo sapiens (Human).
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Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
                             Gaps
                                                                                                                                                                                                            Cyclin Al.

Brachydanio rerio (Zebrafish) (Danio rerio).

Brachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae, Danio.

NCBI_TAXID=7955;
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Bifidobacterium longum.
Batteria, Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=NCC 2705;
MEDDIINE=22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.;
Query Match 65.8%; Score 50; DB 1; Length 465; Best Local Similarity 62.5%; Pred. No. 4.8; Matches 10; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.2%; Score 48; DB 2; Length 390; llarity 56.2%; Pred. No. 9.1; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                         Bauer M.P., Goetz F.W.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02284; Cyclin_C; 1.—
Pfam; PF00134; Cyclin_N; 1.
SMART; SM03385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
Cell cycle; Cell division; Cyclin.
SEQUENCE 390 AA; 43966 MW; 79DD1F8F1201FF9D CRC64;
                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    i- SIMILARITY: Belongs to the cyclin family.
BMBL, AR58045; AR47015.1; -.
GO:0005634; C:nucleus; IEA.
GO; GO:000074; P:regulation of cell cycle; IEA.
InterPro; IPR004670; Cyclin.
InterPro; IPR004567; Cyclin.
LiterPro; IPR004671; Cyclin.
LiterPro; IPR006671; Cyclin.
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254 VGEEYKLRAETLYLAV 269
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                                                             1 IGEEFSRAAEKLYLAV 16
                                                                                                                                                                PRELIMINARY;
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                              Q7T3L6
Q7T3L6;
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Q8G3P3
                                                                                                                                   RESULT 14
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G): G0:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA. G0; G0:0005279; F:amino acid-polyamine transporter activity; IEA. G0; G0:0006852; P:amino acid-polyamine transporter activity; IEA. InterPro; IPR001828; ANF receptor. IEA. InterPro; IPR000709; Leu_Ile_Val_bind. Pfam; PF01094; ANF receptor. 1. CULLEVALBP. Complete protecome. SEQUENCE 395 AA; 41399 MW; BFB76ABDF722D6A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                        Query Match
63.2%; Score 48; DB 2; Length 395;
Best Local Similarity 62.5%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 3; Indels
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196 VGEAFAKAAEKLGLEV 211
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Query Match
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                                                                             November 10, 2004, 14:55:47; Search time 10.6406 Seconds (without alignments) 143.349 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 94,
Sequence 373
Sequence 4,
Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/iaa/5A_COWB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COWB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COWB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COWB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                               478139 segs, 66318000 residues
                                                                                                                                  US-10-092-750-226
117
1 KAEVQIARKLQCIADQFHRLHVL 23
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Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match
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                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                        Scoring table:
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2, Appli 35, Appli 35, Appl 22, Appl 1145, Ap 9, Appli 16, Appli 11, Appli 12, Appli 13, Appli 14, Appli 14, Appli 14, Appli 16, Appli 17, Appli 18, Appli 19, Appli 1	aster	m.	aste r	
28824000044 28824 , , , , , , , , , , , , , , , , , , ,	Bot	Gapi	po d	
sednence Sed	Drosophila melanogaster	. 286; els 2;	phila melanogast	764;
		Length 5, Ind	F Drosophil	Length
2 7 7 8 8	NTS oteins of	DB 4; .7; es	roteins of	DB 4;
9-813-818-2 1454-097-35 9-457-0408-22 9-538-092-114 9-135-984-9 9-135-984-9 9-553-867A-19 9-553-867A-19 9-553-867A-19 9-553-867A-19 9-553-867A-19 9-553-867A-19 9-553-867A-19 9-72-112-1 9-72-112-1 9-72-112-1 9-72-112-1 9-72-112-1 9-72-112-1 9-72-112-1 9-72-112-1 9-73-813-87A-19	7 7 994 7 094	48; No. matc	67 -094 0,76 ino	re 48;
	ALIGN 15/09270767 acids and ace: 7326-0 US/09/270, 1-17	0.0	cation US/092707 et al. Nucleic acids an Reference: 7326 NUMBER: US/09/27 1999-03-17 16217 16217 17 210 210 210 2217 2210 22217 2220 2222	Score
4 H W W 4 W 4 4 4 4 4 4 4 4 4 4 4 4 4 4	on US al. eal. erence erence ER: 1 19-03- 1517 2.0 lanog	. 08 . 08 ADQI	on US al. eeic erencerences 39-03-1 39-03-1 200	41.0%;
409 415 415 415 416 416 416 416 416 428 428 428 428 428 428 428 428 428 428	lication US/0927 er et al. er et al. i. Nuclearic acids R. Number: US/09/ N. NUMBER: US/09/ SE: 1999-03-17 OS: 62517 Ver: 2.0 ila melanogaster xaa means any	41. servative -ARKLQCIA :	ication US r et al. Nucleic a Referenc NUMBER: 1999-03- 1999-03- S: 62517 Ver. 2.0	41.
	767-57322 (57322, Application INCORMATION: NT: Homburger et a. NT: Homburger et a. NT: HOMBURGER EN NOTE: PERENCE: File Necle: APPLICATION NUMBE! TELING DATE: 1999 OF SEQ ID NOS: 625; E: Patentin Ver. 2 (6) 57322 E: Patentin Ner. 2 E: Patentin Ner. 2 E: Patentin Ner. 2 E: Patentin Ner. 2 E: Reference 2 E: Reference 2 E: Reference 2 E: Reference 2 E: Reference 2 E: Reference 2 E: Reference 2 E: Reference 2 E: Reference 3 E:	7-57322 h Similarity 50.0%; Pr. 11; Conservative 4; 2 AEVQI - ARKLQCIADQFHRLH	767-42064 142064, Appl 10. 6703491 INFORMATION: NT. Homburge P. INVENTION: P. FILLING DATE OF SEQ ID NO E: Patentin 10.42064 PRT PRT SM: Drosophi E: SM: Drosophi E: Total PRT SM: Drosophi E: Total PRT SM: Drosophi E: Total PRT SM: Drosophi E: Total PRT Tot	· >
	SULT 1 SULT 1 Sequence 57322, Application US/0927076' Sequence 57322, Application US/0927076' Sequence 57322, Application US/0927076' Sequence 57322, Application US/0927076' Patter No. 670341 TITLE REPRENCE: File Reference: 7326-1 CURRENT APPLICATION NUMBER: US/09/270 CURRENT FILING DATE: 1999-03-17 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 57322 INDE: PRT ORGANISM: Drosophila melanogaster FEATURE: CHERINE: OTHER INFORMATION: Xaa means any amin	.767- atch lal S 11 2		atch
8 6 0 0 11 5 12 14 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ELO:	US-09-270-76 Query Matc Best Local Matches Qy	RESULT 2 US-09-270-767 US-09-270-767 Sequence 422 Patent No. GRNERAL INF ARBERLANT: ITILE OF II TITLE OF II FILE REPER, CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CURRENT API CONTANTAL CO	3

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GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: HOLD AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI)
TITLE OF INVENTION: MOREN: US/09/543,681A
TITLE OF INVENTION: UNMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
SEQ ID NOS: 8344
SEQ ID NO 5913
LENGTH: 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 73, Application US/09228986

Sequence 73, Application US/09228986

Patent No. 6359198

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/A020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
          TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster PILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49430
LENGTH: 806
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37.6%; Score 44; DB 4; Length 806;
Best Local Similarity 44.4%; Pred. No. 68;
Matches 8; Conservative 5; Mismatches 5; Indels
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US-09-270-767-49430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5913, Application US/09543681A Patent No. 6605709
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                                                                                                                                                                                                                                                   ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EVQIARKLQCIADQFHRLHV 22
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APPLICANT: Homburger et al.
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US-09-228-986-73
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Best Local Similarity
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LENGTH: 947
TYPE: PRT
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US-09-252-991A-30629
is Gequence 30629, Application US/09252991A
is Patent No. 6551795
is General Nicormation:
Application US/09252991A
is Patent No. 6551795
is GENERAL INFORMATION:
ADPLICATION:
AUTILE OF INVENTION:
TITLE OF INVENTION:
ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
ITTLE OF INVENTION:
ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER:
US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30629
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Sequence 34213, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 34213

LENGTH: 806

LENGTH: 806
                        Gaps
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38.0%; Score 44.5; DB 4; Length 229;
Best Local Similarity 57.9%; Pred. No. 14;
Matches 11; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 4; Length 806;
Pred. No. 68;
5; Mismatches 5; Indels
                           Indels
                           ъ,
Best Local Similarity 50.0%; Pred. No. 14;
Matches 11; Conservative 4; Mismatches
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US-09-270-767-34213
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670 AEIQVLNIRKYICISEQVIRLH 691
                                                                        2 AEVQI -- ARKLQCIADQFHRLH 21
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| SS KGEVRIARRLIGAQCSPDQ 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KAEVQIARKI---QCIADQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 44.4%;
Matches 8; Conservative
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US-09-270-767-49430
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Gaps

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us-10-092-750-226.rai

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Length 1621;
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Pred. No. 43;
2; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50, Application US/09533029
Patent No. 666446
GENERAL INFORMATION:
APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Ricchman, Jose-Luis
APPLICANT: Ricchman, Jose-Luis
APPLICANT: Pineda, Omaira
APPLICANT: Pamba, Luc
APPLICANT: Pamba, Juc
APPLICANT: Adam, Luc
APPLICANT: Adam, Luc
APPLICANT: Adam, Luc
APPLICANT: Adam, Luc
APPLICANT: ALCIHIE, Oliver
APPLICANT: Yu, Guo-Liang
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Wow One DISEASE-INDUCED POLYNUCLEOTIDES
ITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
CURRENT FILING DATE: 1099-03-23
UURBER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
CONT IN NO. 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43.5; DB 1;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1489 ASVLVVGSLQCISDKQFQHLSV 1510
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Patent No. 6057129
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                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-789-1400
TELEPAX: 713-789-2679
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.2%;
50.0%;
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Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                               LENGTH: 1621 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.03
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-242-677-2
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US-09-533-029-50
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US-09-100-664A-3
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwahuizen, Nicolaas
APPLICANT: Nieuwahuizen, Nicolaas
APPLICANT: Nieuwahuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REPERENCE: 11000.10202
CURRENT FILING DATE: 2002-03-18
FRIOR FILING DATE: 2000-11-01
FRIOR FILING DATE: 1999-01-12
FRIOR FILING DATE: 1999-01-12
FRIOR FILING DATE: 2000-01-11
FRIOR FILING DATE: 2000-01-11
FRIOR FILING DATE: 2000-01-11
FRIOR FILING DATE: 2000-01-11
FRIOR FILING DATE: 2000-01-11
FRIOR FILING DATE: 2000-01-11
FRIOR APPLICATION NUMBER: 60/162,866
FRIOR APPLICATION NUMBER: 60/162,866
FRIOR APPLICATION NUMBER: 60/162,866
FRIOR APPLICATION NUMBER: 90/100724
FRIOR FILING DATE: 2000-01-11
FRIOR APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PATE APPLICATION NUMBER: PAT
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Patent No. 5677143
GENERAL INFORMATION:
APPLICANT: Gaynor, Richard B
APPLICANT: Wi. FOOM W
TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
TITLE OF INVENTION: and Uses Thereof in regulating Gene Expression and in the TITLE OF INVENTION: Treatment of AIDS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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          Length 947;
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                                                                      Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242 for FILING DATE:
      DB 3;
   Query Match
37.2%; Score 43.5; D
Best Local Similarity 43.5%; Pred. No. 99;
Matches 10; Conservative 4; Mismatches
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37.2%; Score 43.5; D
Best Local Similarity 43.5%; Pred. No. 99;
Matches 10; Conservative 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 EVQIARKLQ---CIADQFHRLHV 22
                                                                                                                              3 EVQIARKLQ---CIADQFHRLHV 22
                                                                                                                                                                                                                                                                                                                                                 Sequence 73, Application US/10101464A, Patent No. 6768041
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COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Arnold, Wh
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houston
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US-08-242-677-2
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MS-09-270-767-41050

Sequence 41050, Application US/09270767

Fatent No. 6703491

GENERAL INFORMATION:

SEPPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

CURRENT PEPLICANTON: NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARET PERCENT PERCENTIN Ver. 2.0

SEQ ID NO 41050

LENGTH: 233
                                                                                                                                                                                                                                                                                                                                                          GENERAL INVOKATION:

GENERAL INVOKATION:

APPLICANT: Young, Michael W
APPLICANT: Young, Michael W
APPLICANT: Alau, Justin
APPLICANT: Palau, Justin
APPLICANT: Price, Jeffrey
APPLICANT: Price, Joseph S.
APPLICANT: Philip, Lowrey L.
TILLE OF INVENTION: A NOVER L.
TILLE OF INVENTION: A NOVER C.
CURRENT APPLICATION NUMBER: 000-04-20
PRIOR APPLICATION NUMBER: 000-04-20
PRIOR APPLICATION NUMBER: 000-04-20
PRIOR APPLICATION NUMBER: 09/335,983
PRIOR FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 440
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Best Local Similarity 36.0%; Pred. No. 36;
Matches 9; Conservative 5; Mismatches 5; Indels
                                       DB 4; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.8%; Score 43; DB 4; Length 440; Best Local Similarity 38.9%; Pred. No. 51; Matches 7; Conservative 6; Mismatches 5; Indels
                                36.8%; Score 43; DB
ilarity 38.9%; Pred. No. 51;
Conservative 6; Mismatches
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US-09-270-767-41050
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                                                                                                                                                                                                                                                     RESULT 13
US-09-553-867A-3
; Sequence 3, Application US/09553867A
; Patent No. 6476188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Drosophila melanogaster
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                                                                                                                                     5 QIARKLQCIADQFHRLHV 22
                                                                                                                                                                   34 EVAIKLECIRTKHSQLHI 51
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                                                             Best Local Similarity
Matches 7; Conserva
                                          Query Match
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| Sacquence 3, Application US/09335983
| Patent No. 6436628
| GBNEARAI INPORMATION:
| APPLICANT: Young, Michael W
| APPLICANT: Kloss, Brian
| APPLICANT: Kloss, Brian
| APPLICANT: Price, Joffrey
| TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE THEREOF
| FILE REPERENCE: 600-1-221N
| CURRENT FILING DATE: 1999-06-18
| BARLIER APPLICATION NUMBER: 09/100,664
| BARLIER FILING DATE: 1998-06-19
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 3
| LENGTH: 440
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APPLICANT: BLAU, JUSTIN
APPLICANT: BLAU, JUSTIN
APPLICANT: PICE, JEFFREY
TITLE OF INVENTION: A NOVEL
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klamber
STRRFFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 36.8%; Score 43; DB 3; Length 440; Best Local Similarity 38.9%; Pred. No. 51; Matches 7; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                             COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eleoppy disk
COMPUTER: Eleoppy disk
COMPUTER: Eleoppy disk
COMPUTER: Eleoppy disk
COMPUTER: DEAD COMPUTER: POSSIMS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/100,664A
FILING DATE: 19-JUN-1998
CLASSIFICATION: 435
ATTONREY/AGBRT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REJERRANCE/DOCKET NUMBER: 26,742
REJERRANCE/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 201-343-1684
                                                                                                                                                                                                                               E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT ; ORGANISM: Drosophila melanogaster US-09-335-983-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                        STREET: 411 nec. CITY: Hackensack STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                        COUNTRY: UN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-335-983-3
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RESULT 15
US-09-270-767-56266

1 Sequence 56266, Application US/09270767

2 Sequence 56266, Application US/09270767

3 Sequence 56266, Application US/09270767

3 EXERGIBERE INCEMPATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

CURRENT FILING DATE: 1999-03-17

NUMBER: Patentin Ver. 2.0

SEQ ID NO 56266

LENGTH: 233

TYPE: PRT

CORGANISM: Drosophila melanogaster

PEATURE:

CORGANISM: Drosophila melanogaster

CORGANISM: OFFER INFORMATION: Xaa means any amino acid

US-09-270-767-56266

Query Match

Best Local Similarity 36.0%; Pred. No. 36;

Matches 9; Conservative 5; Mismatches 5; Indels 6; Gaps 1;

Qy 3 EVQIARKLQ-----CIADQPRRLH 21
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Search completed: November 10, 2004, 15:57:24 Job time: 11.6406 secs

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November 11, 2004, 02:43:24 ; Search time 55.5765 Seconds (without alignments) 146.426 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1568699 segs, 353819137 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-092-750-226
117
1 KAEVQIARKLQCIADQFHRLHVL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
. Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_AA:*
                                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	% Query Match Length DB	DB	ΩΙ	Description
	117	100.0		14	US-10-092-750-226	Sequence 226, App
7	57	48.7	157	17	US-10-739-930-10801	Sequence 10801, A
m	53	45,3	79	17	US-10-425-115-329239	Sequence 329239,
4	53	45.3	250	17	US-10-425-115-244863	Sequence 244863,
Ŋ	52	44.4		16	US-10-767-701-60849	Sequence 60849, A
9	52	44.4		17	US-10-425-115-217289	Sequence 217289,
7	51	43.6	8	16	US-10-767-701-42415	Sequence 42415, A
00	47.5	40.6		17	US-10-425-115-276339	Sequence 276339,
σ	47	40.2		15	US-10-424-599-233142	Sequence 233142,
10	46	39.3		16	US-10-437-963-157663	Sequence 157663,
11	45.5	38.9		11	US-09-864-408A-5252	Sequence 5252, Ap
12	45	38.5		17	US-10-425-115-218585	Sequence 218585,
13	4.5	38.5		15	US-10-424-599-202266	Seguence 202266,

, e	Sequence 38232, A	a)	e 60	e 26	e 23	e 376,	e 18131	e 17444	equence 26399	equence 13258	equence 19646	e 4184	e 880	e 196	ω	a 73,	e 203	333	۵	14180	e 28481	e 4223	equence 5336	equence 62916	equence 1333	e 31863	Seguence 67725, A	e 7000	equence 38329	Sequence 284810,
10-424-599-197	-10-278-173-100	-10-278-536-84	0-225-066A-	-10-302-267-2	-10-374-780A-23	-10-412-699	10-437-963-18131	-0-437-96	.0-425-115-26399	.0-437-963-13258	10-424-599-1	0-425-114-418	10-739-930-880	10-424-599-196	US-10-424-599-163333	LO-101-464A-7	10-408-765A-20	10-029-386-3	10-425-115-212	10-437-963-141	10-424-599-2848	10-425-114-	10-425-114-53	10-767-701-6291	10-437-963-13	10-425-115-31863	10-282-122A-	-10-282-122A-700	10-425-114-3832	US-10-424-599-284810
15	1 T	14	14	14	15	15	16	16	17	16	15	15	17	15	12	14	16	14	17	16	15	15	15	16	16	17	15	15	15	12
355	nν	w	9	460	460	460	475	869	9	52	157	385	392	491	588	947	1621	105	121	130	172	172	172	192	214	265	283	283	313	321
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45	4, 4 V R	. 4	45	45	45	45	45	45	44.5	44	44	44	44	44	44	e,	43.5	43	43	43	43	43	43	43	43	43	43	43	43	. 43
14	1 T	17	18	19	20	21	22	23		25		27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

JS-10-092-750-226

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ch 100.0%; Score 117; DB 14; Length 23; Similarity 100.0%; Pred. No. 2.2e-11; 23; Conservative 0; Mismatches 0; Indels (
Sequence 226 Application US/10092750
; Sequence 226 Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
    APPLICANT: Hammond, Philip W.
; APPLICANT: Alpini, Julia
    APPLICANT: Mright, Martin C.
; TILE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REPERBNCE: 20036/050002
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR PELING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOOTHARE: PastSEQ for Windows Version 4.0
; LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KAEVQIARKLQCIADQFHRLHVL 23
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-10-092-750-226
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Best Local S
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Matches
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KAEVQIARKLQCIADQFHRLHVL 23

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; Sequence 10801, Application US/10739930 ; Publication No. US20040216190A1 ; GENERAL INFORMATION: RESULT 2 US-10-739-930-10801

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|:|| | ::| ||| | 118 | 218 QMARSLLAVSDYFHRLRTL 236
                                                                                                                                                                                                                                                                                                                                                                                                       5 OIARKLOCIADOFHRLHVL 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Sorghum bicolor
                    TYPE: PRT
ORGANISM: Zea mays
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US-10-425-115-217289
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US-10-767-701-60849
                                                                                             FEATURE:
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Sequence 3293.9, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa J.
APPLICANT: Cao, Yonda K.
APPLICANT: Cao, Yonda C.
APPLICANT: Cao, Yonda 
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa: Thomas J.
APPLICANT: Los Voralic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 244863
LENGTH: 250
APPLICANT: Kovalic, David K.

TITLE OF INVENTION: NUCLBIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 10801
LENGTH: 157
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Query Match

48.74; Score 57; DB 17; Length 157;
Best Local Similarity 57.94; Pred. No. 0.53;
Matches 11; Conservative 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C71899_1.p
US-10-739-930-10801
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US-10-425-115-329239
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Pred. No. 1.1;
0; Mismatches 7
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Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Zea mays
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US-10-425-115-329239
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                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Sequence 217289, Application US/10425115
; Sequence 217289, Application No. US20040214272A1
; Sequence 217289, Application No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: Last Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
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; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: J8-2163220, Young Mith
; LENGTH: L13
; ENGTH: L13
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 60849, Application US/10767701
Publication No. US20040172684A1
Publication No. US20040172684A1
ARPERZARAL INFORMATION.
APPLICANT: Kovalio.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 60849
LENGTH: 97
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                                                                                             Length 250;
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44.4%; Score 52; DB 17; Length 113;
Best Local Similarity 45.0%; Pred. No. 2.3;
Matches 9; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52; DB 16; Length 97; Pred. No. 2; 0; Mismatches 7; Indels
                                                                                                                                                  Indels
, OTHER INFORMATION: Clone ID: MRT4577_154904C.1.pep
US-10-425-115-244863
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US-10-425-115-217289
                                                                                       DB 17;
3.7;
                                                                                   Query Match
Best Local Similarity 52.6%; Pred. No. 3.7;
Matches 10; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Clone ID: 9298346.pep
US-10-767-701-60849
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Page 3

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 233142

LENGTH: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15763, Application US/10437963
; Sequence 157663, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Pilant
; APPLICANT: Li, Pilant
; APPLICANT: Li, Pilant
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF TOWNERT FILING DATE: 2003-05-14
; UNIVER OF SEQ ID NOS: 204966
; SEQ ID NO 157663
; LENGTH: 519
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Best Local Similarity 36.8%; Pred. No. 1e+02;
Matches 7; Conservative 5; Mismatches 7; Indels
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US-10-437-963-157663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52551C.1.pep
US-10-424-599-233142
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 ÓLVTCVÓCTÁBLYHEMHAL 290
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113 ILRQLQKLAPELHRVHFL 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
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US-10-276339
i Sequence 276339, Application US/10425115
j Publication No. US20040214272A1
j Fublication No. US20040214272A1
j GENERAL INFORMATION:
j APPLICANT: La Rosa, Thomas J.
j APPLICANT: Cao, Yongwei
j APPLICANT: Cao, Yongwei
j TITLE OF INVENTION: Plants
j TITLE OF INVENTION: Plants
j FILE REFREENCE: 38 - 21 (53222) B
j CURRENT APPLICATION NUMBER: 2003-04-28
j NUMBER OF SEQ ID NOS: 369326
j SEQ ID NO 276339
j LENGTH: 65
                                                                                                                                                                                                                                                                                                                                        | Sequence 42415, Application US/10767701
| Sequence 42415, Application US/10767701
| Publication No. US2040172684A1
| GENERAL INPORMATION:
| APPLICANT: Kovalic, David K.
| APPLICANT: Cao, Yindsel
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
| FILE REFERENCE: 38-21(53535)B
| CURRENT APPLICATION NUMBER: US/10/767,701
| CURRENT FILING DATE: 2004-01-29
| SEQ ID NO 42415
| LENGTH: 89
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40.6%; Score 47.5; DB 17; Length 65;
Best Local Similarity 62.5%; Pred. No. 6.7;
Matches 10; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 43.6%; Score 51; DB 16; Length 89; Best Local Similarity 52.6%; Pred. No. 2.6; Matches 10; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C45474_1.pep
US-10-767-701-42415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: MRT4577_183604C.1.pep
US-10-425-115-276339
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                                                                                                                                                                                                                  45 IRLPRQLPCSADHMHHLHDL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 QIARKLQCIADQFHRLHVL 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
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US-10-424-599-233142
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Sequence 1971171930, Application US/10424599
Sequence 197897, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5323)B
FURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 197587
LENGTH: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38292, Application US/10425114

Sequence 38292, Application US/10425114

Publication No. US20040034888A1

SEQUENCE INV. Unidency

APPLICANT: Liu, Unidency

APPLICANT: Zhou, Yihua

APPLICANT: Scoren, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Papaska, Jack E

APPLICAN
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                                                                                                                                                                                                                                                                                                                                                                      Indels
             ; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INPORMATION: Clone ID: PAT_MRT3847_24671C.1.pep
US-10-424-599-202266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_20447C.1.pep
US-10-424-599-197587
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US-10-425-114-38292
                                                                                                                                                                                                                                                                              Query Match 38.5%; Score 45; DB Best Local Similarity 56.2%; Pred. No. 56; Matches 9; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 IARKLQCIADQFHRLH 21
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ORGANISM: Glycine max
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ORGANISM: Glycine max
FEATURE:
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US-10-424-599-197587
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APPLICANT: Shinkets, Richard A.

TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides Enco FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR PLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5252
LENGTH: 119
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: About Yihua
APPLICANT: Covalic David K
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APPLICANT:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Avoid K.
APPLICANT: Avoid Y.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
LENGTH: 62
LENGTH: 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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US-10-425-115-218585
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45.5%; Pred. No. 16;
iive 5; Mismatches 7
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Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 218585, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 AAVQLYRWLEVNLDQYNCIHVL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 IAGKL---ADQFHKKHLL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.9%;
Best Local Similarity 61.1%;
Matches 11; Conservative ;
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Best Local Similarity 45.59
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US-09-864-408A-5252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
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US-10-425-115-218585
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US-10-424-599-202266
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Length 358;

DB 15;

38.5%; Score 45;

Query Match

0; Gaps Best Local Similarity 52.6%; Pred. No. 1e+02; Matches 10; Conservative 2; Mismatches 7; Indels

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Search completed: November 11, 2004, 07:41:47 Job time : 55.5765 secs

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us-10-092-750-226.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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November 10, 2004, 14:52:32; Search time 7.85765 Seconds (without alignments) 281.634 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-092-750-226 117 1 KAEVQIARKLQCIADQFHRLHVL 23

Title: Perfect score: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

``	Description	ostyle	ribose-5-phosphate	hypothetical prote	hypothetical prote	tical	cyclic nucleotide	ed hy	dynein heavy chain	gamma-crystallin 2	gamma-crystallin 2	gamma-C-crystallin	synthe	TRP-185 protein -	retrov	protein F2E2.14 [i	transcription fact	hypothetical prote	phosphoglycerate k	hypothetical prote	probable cyclic nu	ical	hypothetical prote	hypothetical prote	_	Н	U	al	Sp	hypothetical prote
	DI	600	AD0112	G84682	B84631	E85357	T52572	D83069	T18718	CYRTG2	C24060	I83432	A97189	S62356	JC7527	F86353	846523	G96992	T07014	E86294	H86330	T33153	T31778	T05113	T26669	T47847	T03802	9993	209	926
	DB)				Ŋ																								
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	Score	4.8		45		. 45	45	44.5	44			٠	43.5	٠	43	43		43	43	43	43	43	42.5		42	42	42	42		42
Result	No.	н	7	m	4	S	9	7	œ	σ	10	11	12		14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	50

; 0

Gaps

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Query Match
Best Local Similarity 55.6%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 5; Indels

hypothetical prote	glutelin II precur	glutelin 2 precurs	glutelin type I pr	glutelin II precur	glutelin precursor	hypothetical prote	hypothetical prote		hypothetical prote	SOX-LZ - rainbow t	hypothetical prote	major capsid prote	probable spectrin	hypothetical prote	hypothetical prote
S76299	FWRZ2	B34332	806350	A34332	A27033	T22311	T06682	F86143	A85355	151083	T24587	VCBESS	T42993	T23630	B96590
7	Н	~	~	~	7	~	7	N	N	N	~	н	~	N	0
473	499	499	499	499	499	578	705	206	726	767	1295	1330	4063	4101	507
35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.5
	42	42	42	42	42	42	42	42	42	42	42	42	42	42	41.5
42															4,

ALIGNMENTS

·	RESULT 1 T000094 T000094 T000094 Gispedies Ciona intestinalis CjSpecies Ciona intestinalis CjAccession: T00094 A,Reference number: Z14109 A,Reference number: Z14109 A,Reference number: Z14109 A,Reference number: T14109 A,Reference number: T1400 A,Reference number: T1400 A,Reference number: T1400 A,Reference number: T1400 A,Reference number: T1600 A,Reference number: T650 A,Reference Number A,Reference CodA> A,Reference Number A,Reference Numb
	Query Match Best Local Similarity 50.0%; Pred. No. 13; Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0; Qy
	AD0112 Inbose-5-phosphate isomerase (EC 5.3.1.6) [imported] - Yersinia pestis (strain CO92) Cispecies: Yersinia pestis Cispecies: Versinia pestis Cibate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004 Cibate: 02-Nov-2001 #sequence_revision Nov-2001 #text_change 09-Jul-2004 Cibate: 02-Nov-2004 C
	Nature 413, 523-527, 2001 A,Title: Genome sequence of Yersinia pestis, the causative agent of plague. A,Reference number: AB0001; MUID:21470413; PMID:11586360 A,Accession: AD0112 A,Status: preliminary A,Molecule type: DNA A,Residuss: 1-218 <kur> A,Residuss: 1-218 <kur> A,Genetics: references: UNIPROT:Q8ZHH8; GB:AL590842; PIDN:CAC89759.1; PID:g15978986; GSPDB:GR C,Genetics: rpiA C,Superfamily: Haemophilus influenzae ribose-5-phosphate isomerase C,Superfamily: Accession of the content of the conten</kur></kur>

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Gaps

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Conserved hypothetical protein PA4612 [imported] - Pseudomonas aeruginosa (strain PAO1) conserved hypothetical protein PA4612 [imported] - Pseudomonas aeruginosa (strain PAO1) (Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C.Accession: D83069
R.Scover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bridamin, S.; Vuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc A,Reference number: A82950; MuID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rikohler, C.; Merkle, T.; Neuhaus, G. Plant J. 18, 97-104, 1999
Airitle: Characterisation of a novel gene family of putative cyclic nucleotide- and calmon Airitle: Characterisation of Airitle: Characterisation of Airitle: Characterisation of Airitle: Airitle: Characterisation of Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Airitle: Ai
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                                                                                                                                                                                                                                          A.Cross-references: UNIPROT:Q9M0A4; GB:NC_001268; NID:g7269957; PIDN:CAB79774.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cyclic nucleotide and calmodulin-regulated ion channel [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MVID:20083488; PMID:10617198
A;Accession: E85357
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44;
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Pred. No.
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56.2%;
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Best Local Similarity 56.2
Matches 9; Conservative
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Best Local Similarity
Matches 11; Conserv
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A;Molecule type: DNA
A;Residues: 1-733 <STO>
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A,Molecule type: DNA
A,Residues: 1-183 <STO>
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A;Gene: PA4612
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C;Accession: 684682
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Titles: Sequence and analysis of Chromosome 2 of the plant Arabidopsis thaliana.
A;Accession: G84682
A;Accession: G84682
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: E85357
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9SL29; GB:AE002093; NID:g4803955; PIDN:AAD29827.1; GSPDB:GN
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38.5%; Score 45;
Best Local Similarity 60.0%; Pred. No. 4
Matches 9; Conservative 1; Mismatch
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                                                                    109 IARKFICIADESKOVGVL 126
                    23
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|ADELKFVASQFRRLH 575
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                    IARKLOCIADOFHRLHVL
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Best Local Similarity 56.2
Matches 9; Conservative
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A, Molecule type: DNA
A, Residues: 1-678 <STO>
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A;Molecule type: DNA
A;Residues: 1-688 <STO>
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A,Gene: At2g23980
A,Map position: 2
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A,Map position: 2
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Cyammer---ryocattm: norvegicus (Norway rat)

Cyaccession: 183432

Ryben Dunnen, J.T.; van Neck, J.W.; Cremers, F.P.M.; Lubsen, N.H.; Schoenmakers, J.G.G.

Ryben 78, 201-213, 1989

A;Title: Nucleotide sequence of the rat gamma-crystallin gene region and comparison with A;Reference number: 160312; MUID:89378747; PMID:2777080

A;Accession: 183432

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-174 <RES>
A;Cross-references: UNIPROT:P02529; GB:M19359; NID:g203626; PIDN:AAA40983.1; PID:g203629

C;Genetics: A;Gene: CRY-gamma-C

A;Introns: 3/3; 84/3

C;Superfamily: beta-crystallin

C;Keywords: duplication
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                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Nov-1997
C;Accession: C24060
E;Accession: C24060
G;Accession: C14060
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C; Genetics:
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36.0%; Pred. No. 18;
tive 5; Mismatches
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C;Superfamily: beta-crystallin
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 36.0
Matches 9; Conservative
                                                                                    gamma-crystallin 2-1 - rat
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                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: C24060
A;Molecule type: DNA
A;Residues: 1-174 <DEN>
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Cispecies: Rattus norvegicus (Norway rat)
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Cispecies: Rattus norvegicus (Norway rat)
Cipate: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
Cipate: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
Cipate: 13-Jun-1983 #sequence revision 1982
RiMoormann, R.J.M.; den Dunnen, J.T.; Bloemendal, H.; Schoenmakers, J.G.G.
Proc. Natl. Acad. Sci. U.S.A. 79, 6876-6880, 1982
A;Title: Extensive intragenic sequence homology in two distinct rat lens gamma-crystalli
A;Reference number: A93934; MUID:83091061; PMID:6294661
A;Residues: 1-170 eMOO>
A;Cross.references: UNPROT:P02529; GB:J00717; NID:g203632; PIDN:AA40986.1; PID:g203633
C;Superfamily: beta-crystallin repeat (fragment) cG:Superfamily: repeat (GR2>
F;37-79/Domain: crystallin repeat cGR2>
F;84-124/Domain: crystallin repeat cGR3>
F;84-124/Domain: crystallin repeat cGR4>
                                                                                                                                                                                                                                                                                                                                                                                                                       Risims, M.

Rubalted to the EMBL Data Library, October 1996

A; Reference number: 219010

A; Accession: T18718

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-2632 < WIL>

A; Residues: 1-2632 < WIL>

A; Cross-references: UNIPROT: P90736; EMBL: 281028; PIDN: CAB02695.1; GSPDB: GN00023; CESP: BG

A; Experimental source: clone B0365

R; Percy, C.

R; Percy, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: 5
A,Introns: 75/2; 145/2; 312/1; 588/3; 636/1; 668/3; 744/3; 872/3; 1059/3; 1101/2; 1204/2
1; 2632/3
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A;Reference number: Z19722
A;Reference number: Z19722
A;Reference number: Z19722
A;Reference number: Z18724
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rosidues: 1-2632 <WIZ>
A;Residues: 1-2632 <WIZ>
A;Residues: 1-2632 <WIZ>
A;Rosidues: 1-2632 <WIZ>
A;Cross-references: EMBL;Z81096; PIDN:CAB03163.1; GSPDB:GN00023; CESP:B0365.7
A;Baperimental source: clone K03H4
                                                                                                                                                                                                                                               dynein heavy chain homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T18718; T23294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
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Query Match
Best Local Similarity 36.0%;
Matches 9; Conservative 5
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Job time : 8.85765 secs
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A;Molecule type: DNA
A;Residues: 1-384 <STO>
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A;Cross-references: UNIPROT:Q97GM2; GB:AE001437; PIDN:AAK80300.1; PID:g15025354; GSPDB:GA;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2344
                                                                                                                                                                                                                                                                                                                                                                                                                                   TRP-185 protein - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S62356; S77652
R;Nu-Baer, F.; Lane, W.S.; Gaynor, R.B.
R;Nu-Baer, F.; Lane, W.S.; Gaynor, R.B.
A;Title: The cellular factor TRP-185 regulates RNA polymerase II binding to HIV-1 TAR RNA;Reference number: S62356; MUID:96112814; PMID:8846792
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Biochem. Biophys. Res. Commun. 278, 48-57, 2000
Biochem. Biophys. Res. Commun. 278, 48-57, 2000
Ayfulte: Expression of an intracaisternal A-particle-like element in rat ovary.
A,Reference number: GC7527; MUD1:20525406; PMID:11071854
A,Accession: GC7527
A,Accession: GC7527
A,Molecule type: mRNA
A,Residues: 1-365 <GRA>
A,Gross-references: GB:AA964260
G;Comment: This protein is involved in cell proliferation, differentiation, folliculogent C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-1621 <WUB1>
A;Cross-references: UNIPROT:Q13395; EMBL:U38847; NID:g1184691; PIDN:AAC50379.1; PID:g118
A;Style mental source: Hela cells
A;Note: the authors did not translate the codon for residue 557
A;Accession: S77692
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C;Species: Rattus norvegicus (Norvay rat)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7527
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                                                                                                                                              2; Length 368;
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                                                                                                                                                                                                    Indels
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ilarity 50.0%; Pred. No. 1.7e+02;
Conservative 2; Mismatches 8;
                                                                                                                                              DB
                                                                                                                                           37.2%; Score 43.5; Dilarity 45.0%; Pred. No. 38; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 535-556;1404-1427;1535-1548 <WUB2>
C;Keywords: leucine zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                 206 IEICKRLSKISDQF-RFHVV 224
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C;Keywords: ovary; transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
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Matches
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Chin, C.W.; Chung, M.K.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2006
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C. A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Reference number: A86141; MulD:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q39234; GB:AE005172; NID:g9280681; PIDN:AAF86550.1; GSPDB:GN(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                              Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cibate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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47;
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protein F2E2.14 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.8%; Score 43; DB Best Local Similarity 47.4%; Pred. No. 47; Matches 9; Conservative 2; Mismatches
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| QAARGLLALGEYFHRLRAL 372
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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November 10, 2004, 14:50:40 ; Search time 38.5516 Seconds (without alignments) 343.270 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-092-750-226 117 1 KAEVQIARKLQCIADQFHRLHVL 23 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Osnt30 homo sanien	homo	SE O	hon	5 hon	Se cmo	CWO	homo	Aah70043 homo sapi	attus	us	Q8buk0 mus musculu	Q938d4 mycobacteri	Q7u7z4 synechococc	Q72q79 leptospira	Q8f5y3 leptospira	Aas70805 leptospir	044236 ciona intes	Q8wsy4 physarum po	erwinia p	bacillus	Q82tx6 nitrosomona	Q70jz6 bacillus am	Q93i58 bacillus su	S		30	.4	homo sap	Q8ryh6 oryza sativ	Q6btm6 debaryomyce
SUMMARIES		ΩI	OGNT30	OGNTS6	Q96LC9	AAH69328	AAH69505	Q9H7K7	Q6P9F6	œ	AAH70043	Q8K589	Q91ZE9	QBBUKO	Q938D4	Q7U7Z4	972079	Q8F5Y3	AAS70805	044236	Q8WSY4	Овичне	Q45563	RPIA NITEU	Q70JZ6	Q93158	CAE11252	Q6X892	AAQ57530	Q9NTV3	BTCI	88	QGBTM6
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Q9AG65 RIAL_YERPE G6K878 AAO57544 AAO57544 G9FE60 P96033 C93XM5 C93XM5 C89EP7 C61434 C81434 C81434 CG15_ARATH CNG6_ARATH CNG6_ARATH
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## ALIGNMENTS

RESULT 1

O6NT30	
ΩI	Q6NT30 PRELIMINARY; PRT; 184 AA.
	(TrEMBLrel. 27, Creat
	(TrEMBLrel. 27, Last
	. 27, Last
	Bcl2 modifying factor.
	Name=BMF;
	Chordata; Craniata; Vertebrata; E
	ia;
	NCBI TaxID=9606;
RN	[1] _
	SEQUENCE FROM N.A.
	TISSUE=PCR rescued clones;
	MEDLINE=22388257; PubMed=12477932;
	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA K	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
	Jordan H., Moore T., Max S
	Marusina K., Farmer A.A., Rubin G.M., Hong L.,
	Soares M.B., Bonaldo M.F., Casavant T.L.,
	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
	ichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
	S R.A.,
	ahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA B	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
	rzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
_	Jones S.J., Marra M.A.;
	"Generation and initial analysis of more than 15,000 full-length human
	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
	[2]
	SEQUENCE FROM N.A.
	TISSUE=PCR rescued clones;
RAS	Strausberg R.;
	Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
SOS	SEQUENCE 184 AA; 20477 MW; 20178F7489662846 CRC64;
910	
Best	Similarity 95.5%; Pred. No. 4.6e-09;
Matches	21; Conservat

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the myosin V actin motor complex, activated by anoikis."; Science 293:1829-1832(201).
EMBL; AY029254; AAX38748.1; - SEQUENCE 184; AA; 20508 MW; 21479B25CC727853 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH69505 PRELIMINARY; PRT;
AAH69505;
20-MAY-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                            BMF protein.
BMF.
                                                                                                                                                                                                                                                                                        AAH69328
AAH69328;
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AAH69505
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                                                                                                                                                                                                                                              TISSUB-PCR rescued clones;

TISSUB-PCR rescued clones;

MEDINE-2238257; PubMed-1477932;

MEDINE-2238257; PubMed-18.4., Grouse L.H., Derge J.G.,

MISCARI S.F., Zeeberg B.A., Grouse L.H., Derge J.G.,

MISCARI S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

MISCARI S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toophyuki S., Carnhori P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Richards S., Worley K.C., Hale S., Garcia M.G., Glabbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Miting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

M. Jones S.J., Marra M.A.,

M. Jones M. Jones M. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. J. L. 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 4.6e-09;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-PCR rescued clones;
Straumberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC069328; AAH69328.1; -.
SEQUENCE 184 AA; 20480 MW; 21454B241C717853 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                            Last sequence update)
Last annotation update)
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                                           184 AA.
                                                                             Created)
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                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.2%;
                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 95...
Best 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.
                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                               BMF protein.
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                                                              O6NT56
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                                           Q6NT56
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Q96LC9
     RESULT 2
Q6NT56
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WEDLINE-22388257; PubMed=12477932;

XETAUSPERS RESCUES B. A. Grouse L.H., Derge J.G.,

ASTRUBBERS R.L., Feingold B.A., Grouse L.H., Derge J.G.,

REDLINE-22388257; PubMed=12477932;

ASTRUBBERS R.L., Feingold B.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Richards S., Worley K.C., Hale S., Garcia A.M., Gab S., Sanchez A.,

Richards S., Worley K.C., Male S., Sachin S., Wolling A.C., Shevchenko Y., Bouffard G.G.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

An Halessley R.W., Tochman J.W., Geren E.D., Dickson M.C.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ryminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human mouse cDNA sequences."
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                                                                                      Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                      Length 184;
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Local Similarity 95.5%; Pred. No. 4.6e-09;
Los 21; Conservative 1; Mismatches 0; Indels
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=PCR rescued clones;
Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC0693328; AAH69328 1; -.
SEQUENCE 184 AA; 20480 MW; 21454B241C717853 CRC64;
; DB 2; Len.
.4.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-2004 (TrEMBLrel. 27, Created)
20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              184 AA.
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                                                                                      1; Mismatches
                         Score 109;
                                                         Pred. No.
                                                                                                                                                                                    PRT;
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                                                                                                                                             1 KAEVOIARKLOCIADOFHRLHV 22
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                         93.2%;
                         Query Match
Best Local Similarity 95.55
Matches 21; Conservative
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Query Match
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                                                                                                                                                                                                                                                                                     REAL SEQUENCE FROM N.A.

REAL TISSUESPER rescued clones;

MEDINELS-2388257; PubMed=12477932;

REAL STRUBBER R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Alterbul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soarse M.B., Bonaldo M.F., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A., Canadar R.A., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Garimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

R. Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUE-PCR rescued clones;
Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0659505; AAH69505.1; -.
SEQUENCE 184 AA; 20477 MW; 20178F7489662846 CRC64;
   27, Last sequence update) 27, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLJ00065 protein (Fragment)
Name=FLJ00065;
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20-MAY-2004 (TrEMBLrel.
20-MAY-2004 (TrEMBLrel.
Bcl2 modifying factor.
                                                                                                                                         sapiens (Human)
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PubMed=14702039;
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MEDINE-228825; PubMed=12477932; MEDINE-228825; PubMed=12477932; MEDINE-228825; PubMed=12477932; MEDINE-228825; PubMed=12477932; MEDINE-228825; PubMed=12477932; MEDINE-228825; PubMed=12477932; MEDINE-228825; PubMed E.A., Schaefer C.F., Bhat N.K., Ratschul S.F., Zoeberg B., Buecow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., And Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Sapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., A Eronstein M.J., Ugdin T.B., Toshiyviki S., Carninci P., Prange C., A Bronstein M.J., Ugdin T.B., Toshiyviki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Rohards S. Worley K.J., Mackernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Melassley R.W., Touchman J.W., Green B.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S., Razywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
R. Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
R. Tanai H., Kimata M., Matanabe M., Hiraoka S., Chiba Y., Ishida S.,
R. A cono Y., Takiguchi S., Matanabe M., Hiraoka S., Chiba Y., Ishida S.,
R. Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
R. Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
R. Togiya S., Momiyama H., Satoh M., Takani S., Tersakima Y., Saroki O.,
R. Mosagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
R. Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
R. Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
R. Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
R. Yamazaki M., Matanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
R. Yamazaki M., Matanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
R. Kawabata A., Hikili T., Kobatake N., Inagaki H., Shigeta K., Senba T.,
R. Kawabata A., Hikili T., Noguchi S., Itoh T., Shigeta K., Senba T.,
R. Togashi T., Oyama M., Hata H., Matanabe M., Komatsu T.,
R. Togashi T., Oyama M., Hata H., Matanabe M., Komatsu T.,
R. Nakai K., Nagase T., Nomura Y., Ohara O., Isogai T., Sugano S.,
R. Complete sequencing and characterization of 21,243 full-length human
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"Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 36:40-45(2004).
EMBL, AK024412; BABIS762.1; -.
NON TER 1 1 1 1
SEQÜENCE 204 AA; 22708 MW; 5CC72C92664A688C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q6P9F6;
05-UTL-2004 (TrEMBLrel. 27, Created)
05-UTL-2004 (TrEMBLrel. 27, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Name=BMF;
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21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Name=Bmf;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Lausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Bat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Haieh F.X., Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Haieh F.X., Robins R.F., Hong L., Sares M.B., Bonaldo M.F., Carninci P., Prange C., Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Milahy S.J., Richards S., Worley K.C., Hale S., Garden A.M., Gay L.J., Hulyk S.W., Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Yilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketreman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anting M. Marza M., Green E.D., Dickson M.C., Anting M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Addenstalin M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Addenstalin M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                               Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC060783; AAH60783.1; -.
EMBL; BC070043; AAH70043.1; -.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                            match 93.2%; Score 109; DB 2; Local Similarity 95.5%; Pred. No. 6.7e-09; es 21; Conservative 1; Mismatches A.
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14-APR-2004 (TrEMBLrel. 27, Last seq
14-APR-2004 (TrEMBLrel. 27, Last ann
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Best Local Similarity
                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Placenta;
                                                       SEQUENCE FROM N.A.
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                                                                                     FISSUE=Placenta;
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MEDLINE=22388257; PubMed=12477912;

MEDLINE=22388257; PubMed=12477912;

A Itausner R.D., Colline F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetuw K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Zeeberg B., Buetuw K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Brachento M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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A Yilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Bratiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Indels
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070043; AAH70043.1; -.
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                                                                                                                                                                                                                                                                          AAH70043 PRELIMINARY, PRT; 261 AA.
AAH70043;
01-JUN-2004 (TYEMBLrel. 27, Created)
01-JUN-2004 (TYEMBLrel. 27, Last sequence update)
01-JUN-2004 (TYEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Homo sapiens (Human).
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                                                                                                       205 QAEVQIARKLQCIADQFHRLHV 226
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                                                             1 KAEVQIARKLQCIADQFHRLHV
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
BC1-Z modifying factor (Mus musculus 0 day neonate thymus CDNA, RIKEN full-length enriched library, clone:A430110F10 product:BCL-Z MODIFYING PACTOR homolog).
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STRAIN=CS7BL/GJ; TISSUE=Thymus;
MEDIINE=2499374; PubWed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĕ
                                                                                                                       STRAIN=Sprague-Dawley;
MEDLINE=2267518; PubMed=12787069;
Itoh T., Itoh A., Pleasure D.;
"BC1-2-related protein family gene expression during oligodendroglial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN-CS7BL/6J; TISSUE-Thymus;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of, 770 full-length cDNAs.";
Nature 420:563-573 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 185;
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Local Similarity 90.9%; Pred. No. 9.7e-09;
les 20; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                            differentiation.";
J. Neurochem. 85:1500-1512(2003).
EMBL, AFSO(561; AAM28890.1; -
SEQUENCE 185 AA; 20710 MW; A8F8D9FF10AD15B4 CRC64;
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STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=99279233; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
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                             NCBI_TaxID=10116;
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Mammalia;
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RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

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RA Togawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA Togawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA Togawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA Togawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA Togawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

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RA Togawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

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prepare full-length cDNA traries for rapid discovery of new genes.";
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STRAIN-CTSBL64; FLANGULS:
STRAIN-CTSBL64; FLUBWEG=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama V., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
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RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
01-WAR-2014 (TrEMBLrel. 26, Last annotation update)
11-WAR-2014 (TrEMBLrel. 27, Last annotation update)
11-WAR-2014 (TrEMBLrel. 27, Last annotation update)
11-WAR-2014 (TrEMBLrel. 27, Last annotation update)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAN=CS-DEL/66, TISSUE-Heart;
STRAN=CS-DEL/66, TISSUE-Heart;
MEDLINE-99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
"High-Efficiency full-length cDNA cloning.";
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A dachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A ratada S., Furuno M., Hanaqaki T., Hara A., Hashizune W.,
A Hayashida K., Hayatsu N., Hirance T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itch M., Kagawa I., Kasukawa T.,
A Katch H., Kawai J., Kojima Y., Konno H., Konno H., Konno H.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Mumazaki R., Ohno M., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasto R., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takaku-Akahira S., Takeda Y., Tanaka T.,
Submitted (ApR-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; AKO04658; BAC3243.1; ---
R MGD, MGI:2176433; BME:
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                                                                                                                                                                                                STRAIN=C57BL/6J; IISSUB=Heart;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAMN=CS/BL/6J; TISSUB=Heart;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wornalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
XINDEACASIO913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nashi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazawa M., Nishine T., Harada A., Yamamoto R., Matsumco H., Itoh M., Yamamoto R., Matsumco H., Itoh M., A Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Yoncda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Oxazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-fermat sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                     "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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97.2%; Pred. No. 2.1e-08;
97.2%; Pred. No. 2.1e-08;
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GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005515; F:pyrctein binding; IPI.
GO; GO:0005515; F:pyrctein binding; IPI.
SEQUENCE 271 AA; 30071 WW; D4EZ7B0AC0998E98 CRC64;
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SEQUENCE FROM N.A.
STRAIN-CSPIL/60; TISSUE-Heart;
MEDLINE-2108560; Pubmed-11217851;
RIKEN FANTOM CONSORTIUM;
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                                                                                                                                                                                   STRAIN=mc2_155;
Derbyshire K.M., Parsons L.M., DeVost J.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
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MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
Chain P., Lamerdin J.B., Regala W., Allen B.E., McCarren J.,
Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.,
The genome of a motile marine Synechococcus.";
Nature 424.1037-1042(203):
EMBL, BX569691; CAE07349.1;
InterPro; IPR010349; Asparaginase_II.
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                                                  Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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Pred. No. 11;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.9%; Score 49; DB 2; Length 325; 36.4%; Pred. No. 28; ive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF06089; Asparaginase II; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 325 AA; 34588 MW; 72DF0DA9C0C81895 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 AA; 28106 MW; B7F32C59CA4CB081 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
NCBI_TaxID=84588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OMAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypotheital protein.
OrderedLocusNames=SYNW0834;
                                                                                                                                                                                                                                                                                                                                                 GO, GO:0016491; F:oxidoreductase activity; IEA. GO; GO:0018152; P:metabolism; IEA. InterPro; IRR002198; ADH short.
PIEAFPCO; IRR002199; Adh short.
Pfam; PF00106; adh_short; I.
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PRINTS; PROODG0; SDRPAMILY.
PROSITE; PSOODG1; ADH_SHORT; UNKNOWN_1.
Oxidoreductase.
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16 APLEVTLKRGCIAESVHRVHAV 37
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91 VARSVQAIADEFGRIDIL 108
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Putative oxidoreductase.
                                Mycobacterium smegmatis
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Matches 8; Conserv
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RESULT 15

269 AA.

PRELIMINARY;

Q938D4 Q938D4;

RESULT 13 Q938D4

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SEQUENCE FROM N.A.

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STRAIN-Fiocut 11-130;

STRAIN-Fiocut 11-130;

STRAIN-Fiocut 11-130;

Nascimento A.L.T.O., Ko A.I., Martins B.A.L., Monteiro-Vitorello C.B., Marches M.V., Oliveira M.C., Manck C.F.M., Leite L.C.C., Carrer H., Marques M.V., Oliveira M.C., Manck C.F.M., Leite L.C.C., Carrer H., Parto B.S., Ferro M.I.T., Purlan L.R., Gamberini M., Giglioti B.A., Goos-Natto A., Goldman G.H., Goldman M.H.S., Harakava R., Aranka B.E., Lemos M. C.M., Lemos M.V.F., Marino C.L., Nunes L.R., A de Oliveira R.C., Percira G.G., Reis M.S., Schriefer A., Schriefer A., Schriefer M.S., Schr
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                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Best Local Similarity 52.9%; Pred. No. 44;
Matches 9; Conservative 4; Mismatches 4; Indels
                                                      351 AA.
                                                      PRT;
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Q72Q79
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Search completed: November 10, 2004, 15:53:41 Job time: 40.6285 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

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143.349 Million cell updates/sec

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Sequence:

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Scoring table:

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Searched:

Title:

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478139
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents AA:*

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4: /cgn2_6/ptodata/1/iaa/GOMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Seguence 3, Appli	equence 2,	28,	30	106	ednence	21443	equence 433,	19827	ednence	286,	14974	equence 313,	21	54	H	'n	21	Seguence 21, Appl	Sequence 7, Appli	equence 21		9	21	equence 33	equence 4,	Sequence 32, Appl
ID	1 1	-09-228-	-60-	-09-377-2	-09-489-0392	-09-252-	-09-252-991	-09-199-637A-43	1A-19	-09-621-9	-09-673-395A-58	-09-248-	-09-199-637A-313	-09-252-991A-214	-09 - 134	-09-144	-09-144-085-	-08-62	-08-5	-424A-	-09-005-546-	-08-477-669-	-581-	4	-09-357-2	-08-468-55	US-09-357-251-32
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US-09-248-796A-23040 US-09-248-796A-27548 US-08-240-712-18	US-08-4443-890-18 US-08-484-686B-65 US-08-463-160B-66 US-09-058-562-18	PCT-US92-09752-18 US-09-161-241-8 US-09-328-352-4658 US-09-583-110-5045	US-09-252-991A-22048 US-08-240-712-21 US-08-240-712-22 TTG-08-443-890-21	US-08-443-890-22 US-08-484-686B-67 US-08-463-160B-68
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### ALIGNMENTS

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JGENERAL INFORMATION

JEGURANE STARRAWICZ, BRIAN S., Oldroyd, Giles Edward,

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JEGURANE STARRAWICZ, BRIAN S., Oldroyd, Giles Edward,

JEGURANE STARRAWICZ, BRIAN S., Oldroyd, Giles Edward,

APPLICANT: SAIMCHON S., Oldroyd, Giles Edward,

APPLICANT: SAIMCHON S., Oldroyd, Giles Edward,

APPLICANT: SAIMCHON S., Oldroyd, Giles Edward,

APPLICANT: SAIMCHON S., Oldroyd, Giles Edward,

APPLICANTE OF INVENTION: PATHOGEN RESISTANCE

NUMBERS OF EGUINCES: 15

COMPRESSEE: Whinston

STREET: One World Trade Center

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STREET: One World Trade Center

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STREET: North S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow S., Oldrow
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APPLICANT: XIAO, BOO
APPLICANT: XIAO, BOO
APPLICANT: LEAHY, Daniel
APPLICANT: LEAHY, JULEA
APPLICANT: LEAHY, JULEA
APPLICANT: LEAHANA AITHONY
TITLE OF INVENTION NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)
FILE REFERENCE: JULISSO-4
CURRENT APPLICATION NUMBER: US 60/138,426
PRIOR APPLICATION NUMBER: US 60/138,493
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR FILING DATE: 1999-06-10
PRIOR PRIOR DATE: 1999-06-10
PRIOR PRIOR DATE: 1998-08-18
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APPLICANT: Gary Breton et. al

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT PEPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-29

RIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 159
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42.7%; Score 47; DB 4; Length 354;
Best Local Similarity 38.9%; Pred. No. 14;
Matches 7; Conservative 6; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/09377285B
Patent No. 6720175
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: WORLEY, Paul
APPLICANT: TU, Jian
                                                                                                           5; Indels
                                                  Score 47; DB 4
Pred. No. 14;
6; Mismatches
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                                                                                                                                                                                          313 GELKSFLEVLDGKIDDLH 330
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                                                Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
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  US-09-377-285B-28
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APPLICANT: XIAO, Bo
APPLICANT: LEAHY, Daniel
APPLICANT: BENEKEN, JULEA
APPLICANT: BENEKEN, JULEA
APPLICANT: LANAHAN, Anthony
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)
FILE REFERENCE: JUL180-4
CURRENT APPLICATION NUMBER: US/09/377,285B
CURRENT FILING DATE: 1999-08-18
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Starkawicz, B. S. et al.

APPLICANT: Starkawicz, B. S. et al.

TITLE OF INVENTION: and Methods for Plant Pathogen Resistance

TITLE OF INVENTION: and Methods for Plant Pathogen Resistance

TITLE OF INVENTION: and Methods for Plant Pathogen Resistance

TITLE OF INVENTION: and Methods for Plant Pathogen Resistance

CURRENT APPLICATION NUMBER: US/05/228,246

CURRENT FILING DATE: 1996-01-11

FARLIER APPLICATION NUMBER: 08/680,327

FARLIER PILING DATE: 1994-09-22

FARLIER PILING DATE: 1994-09-22

FARLIER PILING DATE: 1994-04-13

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2
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Query Match 45.9%; Score 50.5; DB 2; Length 1824; Best Local Similarity 60.0%; Pred. No. 26; Matches 12; Conservative 3; Mismatches 2; Indels 3
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Best Local Similarity 60.0%; Pred. No. 26;
Matches 12; Conservative 3; Mismatches 2: Tndele 3
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; Sequence 28, Application US/09377285B
; Patent No. 6720175
; GENERAL INFORVATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PELING DATE: 1999-06-10
PRIOR PELING DATE: 1999-06-10
PRIOR PELING DATE: 1999-06-10
PRIOR PELING DATE: 1999-06-10
PRIOR PELING DATE: 1999-06-10
PRIOR PELING DATE: 1999-06-10
PRIOR PELING DATE: 1999-06-10
PRIOR PELING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 72
SSOFWARE: PATENTIN VENENON 3.0
SSOF TANARE: PATENTIN VENENON 3.0
LENGTH: 343
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                                                                                                        3 DVVGFIDELEGAVSDLHRAL 22
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Patent No. 6245510
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US-09-228-246-2
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Sequence 19827, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1999-02-18
PRIOR PELING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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                                                                                 APPLICANT: Grodman, Howard M.
APPLICANT: Grodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Rahme, Laurence G.
APPLICANT: Mahajan-Waklos, Shalina
APPLICANT: Tan. Man-Wah
APPLICANT: Tan. Man-Wah
APPLICANT: Tan. Man-Wah
APPLICANT: Toongalis, John
TITLE OF INVENTION: VIRULENCE AND USES THEREOF
FILE REFERENCE: 00708/381002
CURRENT PAPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 433
LENGTH: 317
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Pred. No. 31;
5; Mismatches
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Best Local Similarity 50.0%; Pred. No. 39;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4100, Application US/09621976; Patent No. 639063; Patent No. 6839063; APPLICANT: Dumas Milne Edwards, J.B.
                                                                Ausubel, Frederick
Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.5%;
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Best Local Similarity 32.33
Matches 10; Conservative
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SEQ ID NO 19827
LENGTH: 377
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US-09-252-991A-19827
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                                                                                                                                                                                                                                                                                             Patent No. 6551795
GENERAL INFORMATION:
APPLICANT:
MATC J. Rubenfield et al.
APPLICANT:
MATC J. Rubenfield et al.
APPLICANT:
MATC J. Rubenfield et al.
APPLICANT:
MATC J. Rubenfield et al.
TITLE OF INVENTION:
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ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Sequence 21443, Application US/09252991A
Sequence 21443, Application US/09252991A
Sequence 21443, Application US/09252991A
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUMBER: 36
CURRENT APPLICATION NUMBER: 05/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21443
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40.5%; Score 44.5; DB 4; Length 178;
Best Local Similarity 32.3%; Pred. No. 16;
Matches 10; Conservative 5; Mismatches 5; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
40.9%; Score 45; DB 4; Length 319;
Best Local Similarity 57.1%; Pred. No. 26;
Matches 8; Conservative 3; Mismatches 3; Indels
                                     Indels
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   Pred. No. 12;
2; Mismatches
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US-09-199-637A-433
; Sequence 433, Application US/09199637A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18150
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64.38;
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126 GFLRELDPDVSDLH 139
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296 FVDRLDGAVGDEYR 309
                                                                                               6 GFIDELEGAVSDLH 19
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Best Local Similarity 64,3
Matches 9; Conservative
                                                                                                                                                                                                                                                     RESULT 6
US-09-252-991A-18150
-- 19160 ADE
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US,69/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21432
LENGTH: 346
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40.0%; Score 44; DB 4; Length 309;
Best Local Similarity 25.6%; Pred. No. 37;
Matches 10; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 346;
42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Aucubel, Frederick
APPLICANT: According, Frederick
APPLICANT: According, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Rahme, Laurence G.
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Teongalis, John
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE OF INVENTION: UNBER: US/09/199,637A
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR FILING DATE: 1999-11-25
NUMBER OF SEQ ID NOS: 437
SEQ ID NO 313
LENGTHALE ASSESED FOR WINGOWS Version 4.0
SEQ ID NO 313
                                                                                                                                                                                                                                                             103 MGDIVGTLLHELTHNLYSAHDSKFYKFLDKLKSRYDDIH 141
                                                                                                                                                                                                                               ---FIDELEGAVSDLH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

Query Match

40.0%; Score 44; DB

Best Local Similarity 42.9%; Pred. No. 42;

Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
2.09-252-991A-21432
; Sequence 21432, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 313, Application US/09199637A Parent No. 6355411; GENERAL INFORMATION: APPLICANT: Ausubel, Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 LGFLLGLQDQLRAAVDDVARA 293
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US-09-199-637A-313
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21432
                               TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                  1 MGDVVG---
                                                                             US-09-248-796A-14974
                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-199-637A-313
     LENGTH: 309
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Sequence 14974, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 586, Application US/09673395A

Patent No. 6620923

GENERAL INFORMATION:
APPLICANT: SPECHT, THOMAS

APPLICANT: HINZMANN, BERND
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: POSENTHAL, ANDRE
TILE REFERENCE: ALBRE-12
CURRENT APPLICATION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 637

SOFTWARE: PATENTING DATE: 2.1

SEQ ID NO 586
LIBNGTH: 249
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40.0%; Score 44; DB 4; Length 154;
Best Local Similarity 45.0%; Pred. No. 16;
Matches 9; Conservative 4; Mismatches 7; Indels
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TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION WIMBER: US/09/621,976
CURRENT APPLICATION WIMBER: US/09/621,976
WIMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
LENGTH: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 DIASSEDDLEAARNELHSAL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 DVVGFIDELEGAVSDLHRAL 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 68.4°
Matches 13; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                       ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -147..-1
US-09-621-976-4100
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US-09-673-395A-586
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NESULT 15
US-09-134-000C-5458

i Sequence 5458, Application US/09134000C

i Patent No. 6617156

i GENERAL INFORMATION:

i APPLICANT Lynn Doucette-Stamm et al

i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

i TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

i CURRENT APPLICATION NUMBER: US/09/134,000C

i CURRENT FILING DATE: 1996-08-13

i PRIOR FILING DATE: 1997-08-15

i NUMBER OF SEQ ID NOS: 6812

i SOFTWARE: Patentin version 3.1

i SEQ ID NO 5458

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Query Match
40.0%; Score 44; DB 4; Length 346;
Best Local Similarity 42.9%; Pred. No. 42;
Matches 9; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.1%; Pred. No. 70;
Matches 8; Conservative 3; Mismatches 6; Indels
                                                                                                                           1 MGDVVGFIDELEGAVSDLHRA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5458
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Search completed: November 10, 2004, 15:57:24 Job time : 10.1779 secs

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November 11, 2004, 02:43:24 ; Search time 53.1601 Seconds (without alignments) 146.426 Million cell updates/sec
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(cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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110
1 MGDVVGFIDELEGAVSDLHRAL 22
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Score Match Length DB ID | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | Description | D

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Length 22; Indels

th 100.0%; Score 110; DB 14; Similarity 100.0%; Pred. No. 4.3e-10; 22; Conservative 0; Mismatches 0;

TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-227

Query Match Best Local ( Matches 23 8 8

RESULT 2
US-10-092-750-61
US-10-092-750-61
; Sequence 61, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:

14	48	m.	σ	14	S-10-286-264-56	ø	
15	48	'n	σ	14	-10-225-068-148	Ψ	
16	48	ω.	494	14	S-10-225-066A-2	eguence	28, App
17	48	ω,	g	14	S-10-3	edneuce	o, Appl
18	48	ω,	σ		S-10-425-91	equence	Appli
19	48	ω,	6		-10-374-780A-21	equence	16. App
20	48	'n	, o		-10-412-69	equence	14, App
21	48	ω.	17		-09-918-715-218	equence	18, App
22	48	'n	17		-10-474-79	equence	18, App
23	48	<u>س</u>	~		-10-372-68	equence	o, Appl
24	48	8	17		-10-734-56	equence	l, Appl
25	47.5	ω.	33		-10-437-963-1132	equence	13212,
26	47	42.7	ß		0-425-114-4018	equence	0181, A
27	47	ď	9		-10-424-599-2835	equence	33577,
28	47	ά.	σ		-10-437-963-13291	equence	32914,
29	47	N	4		-10-192-381-28	equence	3, Appl
30	47	v.	S		-10-192-38	equence	J, Appl
31	47	ζ.	М		-10-374-780A-137	ednence	378, Ap
32	47	ά.	ч		-10-412-69	equence	499, Ap
33	47	8	m		-10-437-963-1032	equence	03217,
34	47	ά.	ß		-10-302-26	equence	5, Appl
35	47	ς.	ß		-10-374-780A-21	equence	128, Ap
36	47	ď.	ß		-10-412-699B-934	ednence	34, App
3.7	47	'n	IJ		-10-412-699B-18	edneuce	370, Ap
38	47	ď	N		-10-425-91	eguence	Appli A
33	46		4		-10-425-115-31128	equence	11287,
40	46	ä	S		0-424-599-27578	equence	75789,
41	46	ä	Γ-		-10-424-599-17041	equence	70417,
42	46		338	16	S-10-437-963-1	ence	163935,
43	46	÷.	~		-10-437-963-15751	equence	57518,
44	46	41.8	0		10-128-714-317	equence	.79, Ap
45	46	•	~	14	-714-817	Sequence 81	
					ALIGNMENTS		
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KESOLT I	250-2	7.0					
Sequence:	e 227,	Applic	tion	18/10	092750		
; Publication No. US200	tion N	on No. US200	3003	2157A1			
	INFOR	MATION					
	ANT: H	ammond	Philip	Z			
	ANT	Alpın,	Julia	Ç			
THEFT OF INVENTION: DO COMPANY	DE TNV	ENTION	Polymenti	. t. t.	les Interactive with BCL-Xl		
	BFEREN	CE: 500	036/0500				
	T APPL	ICATION	N NUMBER	.: US	US/10/092,750		
	T FILL	NG DAT	3: 2002	-03-			
	APPLIC	ATION 1	PRIOR APPLICATION NUMBER: US	us 6	0/274,526		
	FILING	DATE:	2001-03	80-			
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Sequence 14158, Application US/10369493
Sequence 14158, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Squence 19891. Application US/10425115
Squence 19891. Application US/10425115
Squence 19891. Application No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 218891
LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 45.5%; Score S0; DB 15; Length 232; Best Local Similarity 40.9%; Pred. No. 15; Matches 9; Conservative 5; Mismatches 8; Indels
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Best Local Similarity 40.9%; Pred. No. 17;
Matches 9; Conservative 5; Mismatches 8; Indels
APPLICANT: Zhou, Jingdong
APPLICANT: Zhou, Tibusa
APPLICANT: Koval, Yibusa
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecule;
TITLE OF INVENTION: Plants and Uses Thereof for Plant Impr
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 37071
LENGTH: 232
TYPE: PPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Clone ID: LIB3180-055-A2_FLI.pep
US-10-425-114-37071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / OTHER INFORMATION: Clone ID: MRT4577_132128C.1.pep
US-10-425-115-219891
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45.5%; Score 50; DB 9; Length 225;
Best Local Similarity 47.8%; Pred. No. 15;
Matches 11; Conservative 7; Mismatches 3; Indels
                                                                                                                                   APPLICANT: Almonia Amerina C.
APPLICANT: Alght, Julia C.
APPLICANT: Wright, Martin C.
TITLE OF INVENTION: POlypeptides Interactive with BCL-XI
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,526
NUMBER OF SEQ ID NOS: 253
NUMBER OF SEQ ID NOS: 253
SEQ ID NO 61
LENGTH: 22
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
US-10-092-750-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
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Pred. No. 0.019;
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Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGRAA, SATOSHI

APPLICANT: MIZOGUCHI, HIROSHI

APPLICANT: ANDO, SEIKO

APPLICANT: TATEISHI, MIKIRO

APPLICANT: TATEISHI, MASHO

APPLICANT: TATEISHI, MASHO

APPLICANT: TEKDA, MASATO

APPLICANT: TEKDA, MASATO

APPLICANT: TEKDA, MASATO

APPLICANT: TEKDA, MASATO

APPLICANT: SENOH, AKHIRO

APPLICANT: SENOH, AKHIRO

APPLICANT: SENOH, AKHIRO

APPLICANT: TATEISHI NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-125

CURRENT PILING DATE: 2000-12-16

PRIOR PILING DATE: 1999-11-16

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOOTHARE: 225

LENGTH: 225
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; Sequence 37071, Application US/10425114
; Publication No. US20040034886A1
; GENERAL INFORMATION:
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145 GNVMGFLAEDGREPALANIHRAL 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GDVVGFI--DELEGAVSDLHRAL 22
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Best Local Similarity 75.0%;
Matches 15; Conservative
                                                                                                                   APPLICANT: Hammond, Philip W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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US-10-444-599-149605

Sequence 149605, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Avalic David K

APPLICANT: Avalic David K

APPLICANT: Avalic David K

APPLICANT: Avalic David K

TITLE OF INVENITON: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENITON: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223)

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 149605

LENGTH: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Goddman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT PILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14898
LENGTH: 490
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Pred. No. 51;
4; Mismatches 3; Indels
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Pred. No. 51;
4; Mismatches 3; Indels
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43.6%; Score 48; DB 15; Length 233;
Best Local Similarity 36.4%; Pred. No. 31;
Matches 8; Conservative 6; Mismatches 8; Indels
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US-10-424-599-149605
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14898, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14898
       ; LENGTH: 490
; TYBE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14503
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299 GPVKGYLEELEGGVSN 314
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Best Local Similarity 56.2%;
Matches 9; Conservative 4
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Best Local Similarity 56.2%;
Matches 9; Conservative
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ORGANISM: Glycine max
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Publication V. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry C.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS MITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052) B

CURRENT FILING DATE: 2003-02-28

FRIOR RILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 11767
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Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Slater, Yongwei

APPLICANT: Glaen, Xianfeng

APPLICANT: Glaen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14503
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Best Local Similarity 56.2%; Pred. No. 33;
Matches 9; Conservative 4; Mismatches 3; Indels
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Pred. No. 50;
4; Mismatches 3; Indels
FILE REPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14158
LENGTH: 331
                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11767
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288 GPVKGYLEELEGGVSN 303
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Best Local Similarity 56.2%;
Matches 9; Conservative
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TITLE OF INVENTION: POLYNUCLECTIDES FOR SEED TRAIT ALTERATION FILE OF INVENTION: POLYNUCLECTIDES FOR SEED TRAIT ALTERATION FILE OF INVENTION BY BOLYNUCLECTIDES FOR SEED TRAIT ALTERATION FILE OF TRAIT ALTERATION NUMBER: US/10/286,264
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATCHIN Ver. 2.1
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43.6%; Score 48; DB 10; Length 494;
Best Local Similarity 36.4%; Pred. No. 74;
Matches 8; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                APPLICANT: 10, 300

TITLE OF INVENTION: Genes for Modifying Plant Traits IV

TITLE REPERENCE: MBI-0025

CURRENT APPLICATION NUMBER: US/09/934,455

CURRENT FILING DATE: 2001-08-22

PRIOR PILICATION NUMBER: MBI-0022

PRIOR PILING DATE: 2000-11-16

PRIOR PILICATION NUMBER: MBI-0022

PRIOR PILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 516

SEQ ID NO 26

LENGTH: 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reddie, James
APPLICANT: Ricchmann, Jose-Luis
APPLICANT: Ratcliffe, Oliver
APPLICANT: Anng, James
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Pineda, Omalra
APPLICANT: Heard, Jacqueline
APPLICANT: Yu, Guo-Liang
APPLICANT: Adam, Luc
                                                                                                                                                                                                                Reuber, Lynne
Riechmann, Jose Luis
Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Arabidopsis thaliana US-09-934-455-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Arabidopsis thaliana
                                      Heard, Jacqueline
Jiang, Cai-Zhong
                                                                                                                                              Pilgrim, Marsha
Ratcliffe, Oliver
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Pilgrim, Marsha
ubell, Arnold
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US-10-286-264-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 56
LENGTH: 494
TYPE: PRT
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US-10-286-264-56
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 291868, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Diants

TITLE OF INVENTION: Diants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

SEQ ID NO 291868

SEQ ID NO 291868

LENGTH: 316
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US-10-739-910-8810

US-10-739-910-8810

US-10-739-910-8810

Publication No. US20040216190A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
43.6%; Score 48; DB 17; Léngth 450;
Best Local Similarity 36.4%; Pred. No. 66;
Matches 8; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
; OTHER INFORMATION: Clone ID: GLYMA-23APR03-C18243_1.p
US-10-739-930-8810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Clone ID: MRT4577_29270C.1.pep
US-10-425-115-291868
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                                                  1 MGDVVGFIDELEGAVSDLHRAL 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||| |:| :|| ||
14 VGDVHGYITKLESLWSNLQAAL 35
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           1 MGDVVGFIDELEGAVSDLHRAL 22
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-934-455-26
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FEATURE:

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43.6%; Score 48; DB 14; Length 494;

Query Match

; Sequence 26, Application US/0993455; ; Publication No. US20030121070A1 ; GENERAL INFORMATION; ; APPLICANT: Adam, Luc

RESULT 13

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                             0; Gaps
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Best Local Similarity 36.4%; Pred. No. 74;
Matches 8; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mendel aborecombology, inc.
APPLICANT: Mendel aborecombology, inc.
APPLICANT: Rechmann, Jose Luis
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline E.
APPLICANT: Jamay, Cai-Zhong
APPLICANT: Jamay, Cai-Zhong
APPLICANT: Jamay, Cai-Zhong
APPLICANT: Adam, Luc J.
APPLICANT: Bineda, Omaira
APPLICANT: Pineda, Omaira
APPLICANT: S14442002040
CURRENT APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 148
SEQ ID NO 148
LENGTH: DATE
LENGTH: DATE
LENGTH: A94
                             8; Indels
Best Local Similarity 36.4%; Pred. No. 74;
Matches 8; Conservative 6; Mismatches
                                                                                                                                                                                               RESULT 15
US-10-225-068-148
; Sequence 148, Application US/10225068
; Publication No. US20030217383A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Bictechnology, Inc.
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Richmann, Jose Luis
                                                                                                           342 LGDAIDYLKELLQRINDLHNEL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: DOMAIN
LOCATION: (308)...(359)
COTHER INFORMATION: Conserved domain
US-10-225-068-148
                                                                           1 MGDVVGFIDELEGAVSDLHRAL 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Arabidopsis thaliana
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Gaps

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Search completed: November 11, 2004, 07:41:47 Job time: 53.1601 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

November 10, 2004, 14:52:32; Search time 7.51601 Seconds (without alignments) 281.634 Million cell updates/sec Run on:

US-10-092-750-227 Title:

22

110 1 MGDVVGFIDELEGAVSDLHRAL Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	А	ption
1	51	46.4	197	2	A87286	conserved hypothet
7	50.5	45.9	1824	7	T07589	disease resistance
М	50	'n	523	ď	B75467	phosphoribosylamin
4	49	44.5	391	~	T04609	hypothetical prote
S	49	4.	491	7	AC2650	glucose-6-phosphat
9	4.9	4.	503	7	B97432	glucose-6-phosphat
7	48.5	•	141	Н	HATJA	hemoglobin alpha-A
æ	ω,	44.1	144	7	HATR1	hemoglobin I alpha
6	48	43.6	141	٦	HAOWP	hemoglobin alpha c
10	48	43.6	3176	N	CGHU3A	collagen alpha 3(V
11	47	42.7		N	A47486	glutathione transf
12	47	42.7		N	S32425	glutathione transf
13	47	42.7		N	T01024	hypothetical prote
14	47	N	450	N	C86262	F13K23.12 protein
15	47	42.7	528	~	AG2288	GTP-binding protei
16	47	42.7	1200	~	C96025	hypothetical expor
17		42.3	141	Н	HAFXB	hemoglobin alpha c
18	46.5	42.3	141	~	S59496	hemoglobin alpha c
19		42.3	143	Н	\$04589	hemoglobin alpha c
20	46	41.8	187	Ŋ	F70164	grpE protein - Lym
21	46	41.8	233	N	C98188	rome c b
22		41.8	233	N	AF3098	hypothetical prote
23	46	41.8	590	ч	GBBPT4	pro
24	46	41.8	1106	N	A97819	
25	'n	41.4	141	н	HACQ	hemoglobin alpha c
56	'n	41.4	141	N	A25357	hemoglobin alpha c
27	45.5	41.4	141	N	$\sim$	hemoglobin alpha c
28	S.	41.4	141	7	S28934	
29	'n.	41.4	142	Н	HAGY	

hemoglobin alpha c isoleucine-tRNA li	hypothetical prote	ubiquinone/menaqui	cell-division prot	adenylyl cyclase-a	phosphoribosylamin	NADH oxidase (noxB	NADH oxidase (noxB	phaseolin G-box bi	delta l pyrroline-	hypothetical prote	hemoglobin alpha-1	hemoglobin alpha c		hemoglobin alpha c
HACA C64418	AH2123	F72262	AG2025	JC4386	A83729	E69407	G69306	T10861	T03695	D39135	D60515	HABTF	HABTV	HAHOD
4 6	N	(1	<b>~1</b>	7	7	7	7	7	N	7	0	н	٦	П
1039	227	248	300	477	511	632	632	642	716	744	140	141	141	141
41.4	40.9	40.9	40.9	40.9	40.9	40.9	40.9	40.9	40.9	40.9	40.5	40.5	40.5	40.5
45.5	4.5	45	45	45	45	4.5	45	45	45	45	44.5	44.5	44.5	44.5
•														

#### ALIGNMENTS

```
C;Species: Caulobacter crescentus
C;Date: 20.Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession. A87286
C;Date: 20.Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession. A87286
C;Accession. A87286
D; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koloni, N.J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87286
A;Accession: A87286
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A;Acc
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conserved hypothetical protein CC0298 [imported] - Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 2;
Pred. No. 4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CC0298
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#### :|| | |||||||| 145 IGFHLETEEAVSDLHRRM 162 S VGFIDELEGAVSDLHRAL 22 à 셤

disease resistance protein Prf - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Species: May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07589
R;Salmeron, J.M.; Oldroyd, G.E.D.; Rommens, C.M.T.; Scofield, S.R.; Kim, H.; Lavelle, D.7
C[81] 86, 123-133, 1996
A;Title: Tomato Prf is a member of the leucine rich repeat class of plant disease resists
A;Reference number: Z16032; MUID:96291405; PMID:8689679
A;Reference number: Z16032; MUID:96291405; PMID:8689679
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: DAA
A;Residues: L-1824 <SAL>
A;Residues: L-1824 <SAL>
A;Residues: L-1824 <SAL>
A;Residues: L-1824 <SAL>
A;Residues: L-1828 <MIPROT:Q96485; EMBL:U65391; NID:g1513143; PIDN:AAC49408.1; PID:g1515
C;Generics:
C;Generics: atrain Rio Grande
C;Generics: number of the leucine rich repeat class of plant disease resists
A;Reperimental source: strain Rio Grande
C;Generics: number of the leucine rich repeat class of plant disease resists
A;Reperimental source: strain Rio Grande

A;Gene: Prf

A;Map position: 5 A;Introns: 1437/2 C;Keywords: leucine zipper; nucleotide binding

Length 1824; 45.9%; Score 50.5; DB 2; Query Match

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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hemoglobin alpha-A chain - tuatara
C;Species: Sphenodon punctatus (tuatara)
C;Species: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 12-Jul-2004
C;Accession: 301136
C;Accession: S01136
R;Abbasi, A.; Wells, R.M.G.; Brittain, T.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 369, 755-764, 1988
A;Title: Primary structure of the hemoglobins from sphenodon (Sphenodon punctatus, tuata)
A;Reference number: S01136; MUID:89105321; PMID:3214555
                                                                                                                                                                                                                                                                                                                                  A;Cross references: UNIPROT:08UHS9; GB:AE008688; PIDN:AAL41617.1; PID:g17738955; GSPDB:Gh
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucose-6-phosphate 1-dehydrogenase (g6pd) [imported] - Agrobacterium tumefaciens (strair CiSpecies: Agrobacterium tumefaciens C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CyAccession: B97432
Ridochner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title, Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Accession: B97432
A; Accession: B97432
A; Accession: B97432
A; Status: preliminary
A; Residues: 1-503 «KUR»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross_references: UNIPROT:Q8UHS9; GB:AE007869; PIDN:AAK86411.1; PID:g15155545; GSPDB:GN
                                                                                                                                            ster, B.W.
AyItile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2650
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44.5%; Score 49; DB 2; Length 503;
Best Local Similarity 56.2%; Pred. No. 22;
Matches 9; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: zwf
A,Map position: circular chromosome
C,Superfamily: glucose-6-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: AGR C 1065
A,Map position: circular chromosome
C,Superfamily: glucose-6-phosphate dehydrogenase
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A,Residues: 1-141 <ABB>
A,Stresidues: 1-141 <ABB>
A,Stross-efferences: UNIPROT:P10059
C,Superfamily: globin; globin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | |:::||| ||:
311 GPVKGYLEELEGGVSN 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 GPVKGYLEELEGGVSN 314
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nes 9; Conserv
                                                                                                                                                                                                                                                                                                                A; Residues: 1-491 < KUR>
                                                                                                                                                                                                                                                         A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B75467
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary
Molecule type: DNA
A,Residues: 1-523 «WHL>
A,Cross-references: UNIPROT:Q9RW01, GB:AE001940, GB:AE000513; NID:g6458577; PIDN:AAF1044
                                                                                                                                                                                                                                                                                      phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase - Deinococq
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Pred. No. 17;
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Pred. No. 16;
4; Mismatches 6
           60.0%; Pred. No. 52; tive 3; Mismatches
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A;Map position: 1
C;Superfamily: purH bifunctional enzyme
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|36 DMVGFIESLLGSV---HRAL 152
                                                                                             3 DVVGFIDELEGAVSDLHRAL 22
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100 GDIAGFLPEAIGLLSDL 116
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Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain R1
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        Best Local Similarity 60.0%
Matches 12; Conservative
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A;Map position: 4
A;Note: F2009.70
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A;Accession: $24465
A;Molecule type: protein
A;Residues: 574-585;965-937, x',975-976;1306-1325;1361-1377;1381-1401;1473-1506,'X',1508
-1962,'X',1964-1965;2018-2037;2374-2410;2445-2459;2466-2469,'X',2471-2474;2504-2508,'X',;
R;Zanussi, S.; Doliana, R.; Segat, D.; Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 267, 24082-24089, 1992
A;Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain £
A;Reference number: $28776; MUID:93054780; PMID:1339440
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A,Note: parts of this sequence were determined by protein sequencing
R;Weil, D.; Mattel, M.G.; Passage, E.; Van Cong, N.; Pribula-Conway, D.; Mann, K.; Deutzn
A,Title: Clouing and chromosomal localization of human genes encoding the three chains of
A;Reference number: A29848; MUID:88161046; PMID:3348212
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A)Cross-references: GB:M27449; NID:g291919; PIDN:AAA52057.1; PID:g291920
By Part of this sequence was determined by protein sequencing
R,Jander, R.; Rautenberg, J.; Glanville, R.W.

Eur. J. Biochem. 133, 39-46, 1983
By Title: Further characterization of the three polypeptide chains of bovine and human shc
A;Reference number: S26506; WUID:83209648; PMID:6852033
A;Accession: S26510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:P12111; GB:X52022; NID:g3127925; PIDN:CAA36267.1; PID:g312795; PiChu, M.J.; Zhang, R.Z.; Pan, T.; Stokes, D.; Conway, D.; Kuo, H.J.; Glanville, R.; Maye EMBO J. 9, 365-393, 1990
EMBO J. 9, 365-393, 1990
A,Title: Mosaic structure of globular domains in the human type VI collagen alpha-3 chair
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A; Residues: 32-126, AK', 129-136, 'L', 138-236 <ZA2>
A; Cross-references: 32-126, AK', 129-136, 'L', 138-236 <ZA2>
A; Cross-references: GB: S49432; NID: 9260296; PIDN: AAB24261.1; PID: 9260297
R; Chu, M.L.; Mann, K.; Deutzmann, R.; Pribula-Conway, D.; Hsu-Chen, C.C.; Bernard, M.P.;
Eur. J. Biochem. 168, 309-317, 1987
A; Title: Characterization of three constituent chains of collagen type VI by peptide sequal A; Reference number: S00126; MUID: 88029444; PMID: 3665927
                                                                                                                       collagen alpha 3(VI) chain precursor [validated] - human.
N;Contains: collagen alpha 3(VI) chain, splice form A9/N10(-)
C;Species: Homo sapiens (man)
C;Species: L-Nov-1993 #sequence_revision 12-Nov-1999 #text_change 16-Aug-2004
C;Accession: A59140; S13679; S24465; A57083; S28776; S00245; C31952; C29848; S26510; S487;RiChu, M.L.
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A, Residues: 2024-2046;2020-2156, K';2203-2208, X',2210-2211, X',2213-2227;2228-2251;2314
A, Residues: 2024-2046;2020-2156, K';2203-2208, X',2210-2211, Y',2213-2227;2228-2251;2314
A, Cross-references: GE:X06196; NID:930055; PIDN:CAA29557.1; PID:91335034
A, Note: the mRNA portion of the sequence corresponds to residues 2092-2157
R;Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; Deutzmann, R.; Timpl, R.
A, Title: Amino acid sequence of the triple-helical domain of human collagen type VI.
A, Reference number: A31952; WUID:89066644; PMID:3198591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-30,237-313,'CWW',318-322,'AR',326-1815,'FD',1818-1819,'ID',1822-3176 <CH5>
A;Cross-references: EMBL:X52022; NID:g3127925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S13679; MUID:90151612; PMID:1689238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-3176 <CHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to GenBank, May 1998
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A; Residues: 2092-2151 <WEI>
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A; Residues: 2038-2373 <CH4>
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A;Accession: A59140
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A, Residues: 310-328 <ZAN>
A, Accession: S28776
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A; Residues: 1-144 <BOS.
A; Residues: 1-144 <BOS.
A; Residues: 1-144 <BOS.
A; Residues: 1-144 <BOS.
A; Residues: 1-144 <BOS.
A; Residues: 1-144 <BOS.
A; Rouser series two more residues, 32-Asp and 33-Lys, than other fish hemogl c; Superfamily: globin, globin homology
C; Superfamily: globin, globin homology C; Reywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; iron; metallog; 2-144/Domain: globin homology GLB.
F; 2-144/Domain: globin homology GLB.
F; 1/Modified site: acetylated amino end (Ser) #status experimental
F; 61/Binding site: oxygen (His) (distal axial ligand) #status predicted
F; 90/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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A;Accession: S03998
A;Molecule type: protein
A;Residues: 1.141 <KLE>
A;Cross-references: UNIPROT:P14525
A;Cross-references: UNIPROT:P14525
C;Superfamily: globin, Apomology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloproteif; P;2.141/Domain: globin homology <CLE>
F;2.141/Domain: globin homology <CLE>
F;2.141/Domain: globin homology <CLE>
F;2.141/Domain: globin homology (CLE>
F;2.141/Domain: gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hemoglobin I alpha chain - rainbow trout (tentative sequence)
(Species: Oncorhynchus mykiss (rainbow trout)
(Spate: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 12-Jul-2004
(Spate: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 12-Jul-2004
(Spatession: A00248
(R.Bossa, F.; Barra, D.; Petruzzelli, R.; Martini, F.; Bruncri, M.
(Bacchim, Biophys. Acta 536, 298-305, 1978
(A)Title: Primary structure of hemoglobin from trout (Salmo irideus). Amino acid sequence
(A)Reference number: A003448; MUID:79042280; PMID:708770
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotei
$2-141/bonain: globin homology cGLB>.
F;58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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C;Species: Bradypus tridactylus (pale-throated sloth)
C;Date: 1190 #sequence_revision 31-Dec-1990 #text_change 12-Jul-2004
C;Accession: S03998
R;Kleinschmidt, T.; Maerz, J.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 370, 303-308, 1389
A;Tile: The primary structure of pale-throated three-toed sloth (Bradypus tridactylus, A;Reference number: S03998; MUID:89335258; PMID:2757790
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                                                                                                                                                                                                                                                                ; DB 1; Length 141; 6.6;
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Pred. No. 7.8;
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Best Local Similarity 50.0%;
Matches 11; Conservative
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                     Query Match
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <COM>
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                                                                                                                                                                                                                                                                                             Accession: B47486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S36782
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A, Residues: 'SAIAGVAGVG' <JAN>
A, Residues: 'SAIAGVAGVG' <JAN>
A, Note: this sequence cannot be reliably placed and probably represents the results from R; Mayer, U.; Poeschl, E.; Nischt, R.; Specks, U.; Pan, T.C.; Chu, M.L.; Timpl, R. Eur. J. Blochem. 225, 573-580, 1994
Eur. J. Blochem. 225, 573-580, 1994
Eur. J. A, Title: Recombinant expression and properties of the Kunitz-type protease-inhibitor mod A; Reference number: $48709; MUID:95045506; PMID:7525281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Map position: 2037.3-2037.3
C.Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA) sociations among trimer amino- and carboxyl-terminal domains (with disulfide bonds).
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Best Local Similarity
Matches 9; Conserv
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A) Experimental source: testis
R; Comstock, K.E.; Widersten, M.; Hao, X.Y.; Henner, W.D.; Mannervik, B.
R; Comstock, K.E.; Widersten, M.; Hao, X.Y.; Henner, W.D.; Mannervik, B.
Axch. Biochem. Biophys. 311, 487-495, 1994
A; Title: A comparison of the enzymatic and physicochemical properties of human glutathior A; Reference number: 845684; MUID:94263230; PMID:8203914
A; Contents: annotation
R; Taylor, J. Bs.; Oliver, J.; Sherrington, R.; Pemble, S.E.
Biochem. J. 274, 587-593, 1991
A; Title: Structure of human glutathione S-transferase class Mu genes.
A; Reference number: 137438; MUID:91174774; PMID:2006920
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Bochem. J. 294, 373-380, 1993
A;Title: Molecular Cloning and heterologous expression of an alternatively spliced human
A;Reference number: S36782; MUID:93384505; PMID:8373352
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human NiAlternate names: glutathione transferase mu4 (Species in the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the const
glutathione transferase (EC 2.5.1.18) class mu, GSTM4 (version 1) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: O2-Jun-1995 #sequence revision 02-Jun-1995 #text_change 09-Jul-2004 C;Accession: A47486; B47486; B36782; I37438; S45685 R;Cometock, K.E.; Johnson, K.J.; Rifenbery, D.; Henner, W.D. J. Biol. Chem. 268, 16958-16965, 1993 A;Title: Isolation and analysis of the gene and cDNA for a human mu class glutathione A;Reference number: A47486; MUID:93352467; PMID:8349586
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A;Molecule type: mRNA
A;Residues: 1-218 <CO2>
A;Cross-references: GB:M96234; NID:g306818; PIDN:AAA57347.1; PID:g306819
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A,Cross-references: EMBL:X56837; NID:g31936; PIDN:CAA40167.1; PID:g31937
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Pred. No. 17;
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A,Emp position: 1p13.3-1p13.3
A,Introne: 12/3; 38/1; 59/3; 87/1; 120/3; 152/3; 189/3
C;Superfamily: glueathione transferase
C;Keywords: alternative splicing; dimer; transferase
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149 VGDKITFVDFLAYDVLDLHR 168
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Best Local Similarity 50.0%;
Matches 10, Conservative
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A;Molecule type: mRNA
A;Residues: 1.218 < ROS>
A;Cross-references: EMBL:M99422
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Gaps

1948 VIHFTDGADGDLADLHRA 1965

RESULT 11 A47486

4 VVGFIDELEGAVSDLHRA 21

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Search completed: November 10, 2004, 15:55:10 Job time : 8.51601 secs
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Best Local Similarity 52.6%;
Matches 10; Conservative
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                                                   A, Map position: 1
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    C;Genetics:
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                                     A,Cross-references: UNIPROT:Q03013, EMBL:X68677; NID:g31934, PIDN:CAA48637.1, PID:g319335
A,Note: the authors translated the codon AAG for residue 182 as Arg and CCA for residue C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetics C,Genetic
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F18K23.12 protein - Arabidopsis thaliana (mouse-ear cress)
F18K23.12 protein - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86262
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzaberg, S.L.; Schwartz, J.C.; Davis, R.W.
A;Authors: Salzaberg, S.L.; Schwartz, J.C.; Davis, R.W.
A;Althe: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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C;Genetics:
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A;Cross-references: UNIPROT:Q9LFW3; GB:AE005172; NID:g8698734; PIDN:AAF78492.1; GSPDB:GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Introns: 101/1
C;Superfamily: Arabidopsis thaliana hypothetical protein YUP8H12R.7
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Pred. No. 32;
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42.7%; Score 47; DB
Best Local Similarity 50.0%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-388 <THE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 VGDKITFVDFLAYDVLDLHR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGDVVGFIDELEGAVSDLHR 20
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Best Local Similarity 53.3%;
Matches 8; Conservative
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14 GTTEELQGCVNDVHR 28
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A;Residues: 1-218 <ZHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: ATSP:YUP8H12R.7
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GYP-binding protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. pCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Species: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG2288
B;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21592285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-528 «KUR»
A;Cross-references: UNIPROT:Q8YQG9; GB:BA000019; PIDN:BAB75561.1; PID:g17132996; GSPDB:G?
A;Experimental source: strain PCC 7120
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                                                                  Gaps
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Query Match 42.7%; Score 47; DB 2; Length 450; Best Local Similarity 36.4%; Pred. No. 38; Matches 8; Indels Matches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 528;
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Pred. No. 4
                                                                                                                                                                  302 LGDAIDYLKELLQRINDLHTEL 323
                                                                                                                         1 MGDVVGFIDELEGAVSDLHRAL 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DVVGFIDELEGAVSDLHRA 21
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 14:50:40; Search time 36.8754 Seconds (without alignments) 343.270 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-092-750-227 110 1 MGDVVGFIDELEGAVSDLHRAL 22

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 Total number of hits satisfying chosen parameters:

1825181 seqs, 575374646 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	nejas como la posición de la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la como la c	1469 salmo		083hp0	Q9pvm4	Q6y257	Aap2019	Q6x9v9 hordeum vul		Aap75622 hordeum v	Q9abdl caulobacter	Q8q0a2 methanosarc	Q73q16 treponema d			Q96485 lycopersico	Q911d0 lycopersico			υ				_			Q8fth9 corynebacte		N	Q8uhs9 agrobacteri
ID		091469	Q83G19	Q83HP0	HBAA SERQU	Q6Y2 <u>5</u> 7	AAP20155	6X6X9Q	AAP75621	AAP75622	Q9ABD1	Q8Q0A2	073016	AAS11123	Q911D4	096485	091160	Q6M5C6	CAF21463	OBNOIO	PUR9 DEIRA	Q8EJV1	Q7V8P0	OPWI0	Q8D3K6	Q7MF16	Q8FTH9	049448	G6PD RHIME	O8UHS9
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Length	22	143	603	603	142	143	143	318	318	318	197	425	646	646	1824	1824	1825	194	194	225	510	554	1057	65	204	221	199	391	491	491
% Query Match	55.5	48,6	•	47.7	•	•	•	•		46.8	46.4		46.4	46.4	45.9		٠	45.5	•	•	45.5	•	•	•	•	•	•	44.5	•	44.5
Score	61	53.5	N	N	Н	51.5	н	ч	⊣	н	51	51	51	51	0	50.5	0	20	50	20	20	20	20	σ	49.5	σ	49	49	49	49
Result No.	-	(1)	٣	4	ហ	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30

07d148 agrobacteri P10059 sphenodon p Q81919 cyprinus ca Q98974 oncorrynchu Q92015 salmo salar P02019 oncorrynchu P14525 bradypus tr Q61pd4 photobacter Cag20842 photobact Q80vvc xenopus lae	Q6h104 capsella bu Q91se2 arabidopsis Q7qai7 anopheles g P12111 homo sapien
Q7D148 HBA_SPHPU Q80H31 Q980H4 Q92015 HBA_CNCMY HBA_BRATR QGLPD4 QGLPD4 QGLPD4	Q6H104 ICE1_ARATH Q7QAI7 CA36_HUMAN
01000111000	4444
503 1441 1443 1443 1444 177 475	492 494 1012 3176
4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6.84.44.66.66.66.66.66.66.66.66.66.66.66.66
4 4 4 4 4	4444
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 4 2 6 4 7

## ALIGNMENTS

RESULT 1  Og65A7  D CG65A7  D CG65A7  D CDEC-2001 (TTEMBLEE1 19, Las) DT 01-DEC-2001 (TTEMBLEE1 19, Las) DE Rel-XL-binding protein v18 (Fragos Mommalia; Etheria; Primates; C  NADITARYOUS FROW N.A.  RY MEDLINE-21293069; PubMed=112830 RX MEDLINE-21293069; PubMed=112830 RX MEDLINE-21293069; PubMed=112830 RX MEDLINE-21293069; PubMed=112830 RX MEDLINE-21293069; PubMed=112830 RX MEDLINE-21293069; PubMed=112830 RX MEDLINE-21293069; PubMed=112830 RX MEDLINE-21293069; PubMed=112830 RX MEDLINE-21293069; PubMed=112830 RX MEDLINE-2129306; Premaire 0) RX MEDLINE-2004 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01, Las) DT 01-NOV-1996 (TTEMBLEE1 01,	70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-60-57  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78  70-78
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MEDINE=22784088; PubMed=12902375;
Racult D., Ogata H., Audic S., Robert C., Suhre K., Drancourt M., Claverie J.-M.;
Claverie J.-M.; Twist: a human pathogenic Actinobacteria with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003896; F:DNA primase activity; IEA.
GO; GO:0016779; F:nucleolidyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006260; F:DNA modification; IEA.
GO; GO:0006260; P:DNA replication; IEA.
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m
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                                                                                                                                                                                                           Query Match

48.6%; Score 53.5; DB 2; Length 143;
Best Local Similarity 54.5%; Pred. No. 8.5;
Matches 12; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Name-dnaG, OrderedLocusNames=TWT288;
Tropheryma whipple! (strain Twist) (Whipple's bacillus).
Macrococineae, Actinobacteria, Actinobacteria, Actinomycetales;
Micrococineae, Cellulomonadaceae, Tropheryma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.7%; Score 52.5; DB 2; Length 603; 46.2%; Pred. No. 47; ive 3; Mismatches 6; Indels 5
         HSSP; P02019; CUT.

GO; GO:0005334; C:hemoglobin complex; IEA.

GO; GO:0005344; F:oxygen transporter activity; IEA.

GO; GO:0015641; P:oxygen transport; IEA.

GO; GO:0015641; P:oxygen transport; IEA.

GO; GO:0015611; P:oxygen transport; IEA.

InterPro: IPR003318; Alpha haem.

InterPro: IPR003019; Globin.

InterPro: IPR003050; Globin.

InterPro: IPR003050; Globin.

InterPro: IPR004051; Globin.

Pfam; PF00401; Globin; I.

PRINTS; PR00612; ALPHAHAEM.

PRINTS; PR00615; PIHAEM.

PRINTS; PR00615; GLOBIN; I.

Heme; Oxygen transport; Transport.

SEQUENCE 143 AA; 15141 MW; 6404A28956019EC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREMA, TIGRO1391; dans. 1. Complete proteome; Nucleotidyltransferase, Transferase. SEQUENCE 603 AA; 67692 MW; 2E5502DA58D28072 CRC64;
                                                                                                                                                                                                                                                                                                                                                   603 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006295; DNA primase.
InterPro; IPR00647; Toprim dom.
InterPro; IPR00647; Toprim primase.
InterPro; IPR002694; Znf CHC2.
Pfam, PP01751; Toprim; 1.
ProDom; PD002276; Toprim; 2.
ProDom; PD002276; Toprim primase; 1.
ProDom; PD00288; Znf CHC2; 1.
TIGRFAMS; TIGR01391; dnag; 1.
                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                             68 IGNAVGLIDDLVGGLSALSDLH 89
                                                                                                                                                                                                                                                               1 MGDVVGFIDELEG---AVSDLH 19
 EMBL; X97286; CAA65949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 46.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=203267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   Q83G19
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ANDLINE-2495039; PubMed=12606174;

RX MEDLINE-22495039; PubMed=12606174;

RAD Bentley S.D., Maiwald M., Murphy L.D., Pallen M.J., Yeats C.A.,

Bentley S.D., Maiwald M., Murphy L.D., Pallen M.J., Yeats C.A.,

Bover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,

Bover L.G., Morbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,

RAD Barrell B.G., Parkhill J., Relman D.A.;

RAD Barrell B.G., Parkhill J., Relman D.A.;

RY "Sequencing and analysis of the genome of the Whipple's disease

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RY Barcel B.G., Farkhill J., Relman D.A.;

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RY GO; GO:000369; F:DNA moidication; EA.

RY GO; GO:0006209; P:DNA moidication; Synthesis of RNA primer; IEA.

RY Probom; PRO1051; Toprim primase; 1.

RY Probom; PRO1051; Toprim primase; 1.

RY Probom; PRO1051; Toprim primase; 1.

RY RY SWO419; TOPRIM; 1.

RY RYART; SWO4040; ZNE CHCC; 1.

RY RYART; SWO4040; ZNE CHCC; 1.

RY RYART; SWO4040; ZNE CHCC; 1.
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16-OCT-2001 (Rel. 40, Last sequence update)
05-UTD-2004 (Rel. 44, Last annotation update)
Hemoglobin alpha-A chain.
Mame-HBAA,
Seriola quinqueradiata (Five-ray yellowtail).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
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Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococáineae; Cellulomonadaceae; Tropheryma.
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46.2%; Pred. No. 47;
tive 3; Mismatches 6; Indels
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Complete proteome; Nucleotidalytransferase; Transferase.
SRQUENCE 603 AA; 67692 WW; 2E5502DA58D28072 CRC64;
                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) DNA primase (EC 2.7.7.-).
                                                                                                                                                                                                                                                                     603 AA.
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2 GDVVGFIDELEG----AVSDLHRAL 22
                                        2 GDVVGFIDELEG----AVSDLHRAL 22
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                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                     PRT;
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Matches 12; Conservative
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Q83HP0;
01-JUN-2003 (
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Q9PVM4;
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Heme; Oxygen transport; Transport.
SEQUENCE 143 AA; 15701 MW; FDCA7EBD81968DFE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Carangoldei;
Carangidae; Seriola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                       TISSUE=Kidney;
Sakai M., Okamoto K.;
"Yellowtail's mRNA for hemoglobin alpha chain A.";
"Yellowtail's mRNA for the EMBL/GenBank/DDBJ databases.
"Le FUNCTION: Involved in oxygen transport from the lung to the various peripheral tissues.
"Various peripheral tissues.
"STBUNIT: Heterotetramer of two alpha chains and two beta chains.
"ITSSUE SPECIFICITY: Red blood cells.
"INSUE SPECIFICITY: Red blood cells.
"INSUE SPECIFICITY: Delongs to the globin family.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha, Acanthopterygii; Percomorpha; Perciformes; Percoldei;
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InterPro; IPR002336; Alpha haem.
InterPro; IPR002031; Globin.
InterPro; IPR009050; Globin.like.
InterPro; IPR009050; Globin.like.
PRIMTS; PR00642; Globin.l.
PROSITE; PS01033; GLOBIN; 1.
FROSITE; PS01033; GLOBIN; 1.
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FROSITE; PS01030; GLOBIN; 1.
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AN190679; AAP20155.1; -.
InterPro; IPR002318; Alpha haem.
InterPro; IPR002011; Globin.
InterPro; IPR009050; Globin.like.
Pfam; PF00042; Globin, 1.
PRINTS; PR00612; ALPHATAEM.
PROSITE; PS01033; GLOBIN; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
1 Alpha hemoglobin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.8%; Score 51.5; DB 1; 54.5%; Pred. No. 17;
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Best Local Similarity 54.5
Matches 12; Conservative
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NCBI_TaxID=143350;
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=8161;
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TISSUE=Spleen;
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SEQUENCE FROM N.A.

MEDLINE=229489313; Pubmed=14586469;

MEDLINE=229489313; Pubmed=14586469;

Collins N.C., Thordal-Christensen H., Lipka V., Bau S., Kombrink E.,

Qui O.L., Huckelhoven R., Stein M., Freialdenhoven A.,

Qui O.L., Huckelhoven R., Stein M., Freialdenhoven A.,

A Somerville S.C., Schulze-Lefert P.;

"SNARE-protein-mediated disease resistance at the plant cell wall.";

"SNARE-protein-mediated disease resistance at the plant cell wall.";

Nature 425:973-977 (2003).

"In Nature 425:973-977 (2003).

"In SMBL; A2468906; AAP75622.1;

"In RemBL; A2468906; AAP75621.1;

"In InterPro; IPR006011; Syntaxin."

REMBL; PROMOSO11; Syntaxin.

REMBL; PROMOSO11; PROMOSO11; T.SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pagrus major (Red sea bream) (Chrysophrys major).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;

NCBI Taxib=143350;
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TISSUB-Spleen;
Chen S.L., Xu M.Y.;
"Analysis of expressed genes in red sea bream (Chrysophrys major).";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY190679; AAP20155.1; -
SEQUENCE 143 AA; 15701 MM; FDCA7EBD81968DFE CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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Length 143;
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AAP20155,
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
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Last annotation update)
   2;
Score 51.5; DB Pred. No. 17; 3; Mismatches
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54.5%; Pred. No. 17;
tive 3; Mismatches
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                                                                                                                  1 MGDVVGFIDELEGA---VSDLH 19
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(TrEMBLrel. 27, I
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Local Similarity 54.5%;
hes 12; Conservative
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hes 12; Conservative
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Length 318;

DB 2;

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EMBL; AY246907; AAP75622.1; -.
SEQUENCE 318 AA; 34547 MW; 908E40B242CE0C39 CRC64;
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STRAIN-GOel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
                                                                                                                                  46.8%; Score 51.5; 1
45.8%; Pred. No. 36;
                                                                                                                       Query Match
Best Local Similarity 45.8%
Matches 11, Conservative
Nature 425:973-977(2003).
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum; Hordeum vulgare.
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Collins N.C., Thordal-Christensen H., Lipka V., Bau S., Kombrink E., Qiu J.L., Huckelhoven R., Stein M., Freialdenhoven A., Somerville S.C., Schulze-Lefert P.;
"SNARE-protein-mediated disease resistance at the plant cell wall.";
Nature 425:973-977(2003).
EMBL, AY246906; AAP75621.1; -.
SEQUENCE 318 AA, 34547 MW; 908E40B242CE0C39 CRC64;
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MEDLINE=22948933; PubMed=14586469;
Collins N.C., Thordal-Christensen H., Lipka V., Bau S., Kombrink B., Qiu J.L., Huckelhoven R., Stein M., Freialdenhoven A., Somerville S.C., Schulze-Lefert P.;
"SNMER-protein-mediated disease resistance at the plant cell wall.";
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Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, Pooideae,
Triticeae, Hordeum, Hordeum vulgare.
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46.8%; Score 51.5; DB 2; Length 318;
Best Local Similarity 45.8%; Pred. No. 36;
Matches 11; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                    Indels
                            Pfam; PF00804; Syntaxin; 1.
SWART; SM0503; SynN; 1.
SWART; SM00397; L SNARE; 1.
PROSITE; PS00914; SYNN; 1.
PROSITE; PS550192; T SNARE; 1.
SEQUENCE 318 AA; 34547 NW; 908B40B242CE0C39 CRC64;
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pfam; PF05739; SNARE; 1
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NCBI_TaxID=112509;
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Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
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61.1%; Pred. No. 27;
ive 2; Mismatches 5; Indels
      Indels
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Pfam, PR0903; Glyoxalase; 1.
Complete protecome; Hypothetical protein.
SEQUENCE 197 AA; 21365 MW; 68ED283154210409 CRC64;
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Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                      197 AA
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7; Mismatches
                                                                                                206 GEVLGVVAEIQERHGAVADLERSL 229
                                                              2 GDVVGFIDELE---GAVSDLHRAL 22
                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Hypothetical protein CC0298.

OrderedLocusNames=CC0298;
Caulobacter crescentus.
                                                                                                                                                                                                                                                                      PRT;
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nes 11; Conservative
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OrderedLocusNames=MM0235;
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RABERARA RABERA 
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 35405 / DSM 14222;

RAS PubMed=15064399;

RAS Beshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,

RAS Beshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,

RAS Belengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J., Durkin S.A.,

Belengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J., Durkin S.A.,

Belengut J., Ren Q., Shetry J., Shvarsman S., McLeod M.P.,

Rasis D., Howell J.K., Pal S., Amin A., Vashisth P., McNeill T.Z.,

Rang Q., Sodergren E., Baca E., Weinstock G.M., Norris S.J.,

Raser C.M., Paulsen I.T.;

R. "Comparison of the genome of the oral pathogen Treponema denticola

with other spirochete genomes.";

Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).

R. FIGR; TDE0628;
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Mol. Plant Microbe Interact. 15:281-291 (2002).
EMBL; AF220602; AF76308.1; ---
GO; GO:0005224; F:ATP binding; IEA.
GO; GO:0005224; F:ATP binding; IEA.
GO; GO:0005229; P:Gefense response to pathogen; IEA.
InterPro; IPR001916; Glyco.hydro.22.
InterPro; IPR001916; Glyco.hydro.22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon pimpinellifolium (Currant tomato).
Bukaryota, Viidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudioctyledons, core eudicots, asterids,
lamids, Solanales, Solanaceae, Solanum.
                                                                                                                                                                  Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21948620; PubMed-11952131;
Chang J.H., Tai Y.S., Bernal A.J., Lavelle D.T., Staskawicz B.J.,
Michelmore R.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.8%; Pred. No. 84;
Matches 11; Conservative 6; Mismatches 5; Indels
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PROSITE; PSO1128; LACTALBUMIN LYSOZYME; UNKNOWN 1.
SROUENCE 1824 AA; 209573 MW; 1F14E7D662DE6AC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528; -.
646 AA; 69759 MW; 2A6IE0B4C74F06C8 CRC64;
                                           OSILID4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
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                PRELIMINARY;
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MEDLINE=22120827; PubMed=12125824; Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A., Deppenmeier U., Johann A., Hartsch T., Merer A., Baeumer S., Jacobi C., Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S., Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P., Fritz H.-J., Gottschalk G., The Genome of Methanosarcina mazei: evidence for lateral gene transfer between Bacteria and Archaea."; J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRIN=ATCC 35405 / DSM 14222;

STRIN=ATCC 35405 / DSM 14222;

STRIN=ATCC 35405 / DSM 14222;

A PubMed=15064399; DOI=10.1073/pas.0307639101;

A Selendri R., Wyers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,

A Selengut J., Ren Q., Erinkac L.M., Madupu R., Kolonay J.F.,

Durkin S.A., Daugherty S.C., Shetty J., Shwattsbeyn A.,

A Shatsman S., McLeod M.P., Smajs D., Howell J.A., Ayodeji B.,

A Shatsman S., McLeod M.P., Smajs D., Howell J.X., Pal S., Amin A.,

Vashisth P., McHold M.P., Xiang Q., Sodergren E., Baca E.,

Mchother spirochete genome of the oral pathogen Treponema denticola

T. Comparison of the genome of the oral pathogen Treponema denticola

T. Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).

PROS. Natl. AROH S. Massill S.J., Fraser C.M., Paulsen J.T.,

Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).

T. TIGR: TDE0628;

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TIGR: TDE0628;
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Н.
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Mame-diak, OrderedLocusNames=TDE0628;
Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=158;
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                                                                                                                                                                                                                                                                                                     / Match 46.4%; Score 51; DB 2; Length 425; Local Similarity 50.0%; Pred. No. 57; Loss 10; Conservative 3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro, 12001023; Hsp70.
Pfam; PF00012; Hsp70; 1
PRINTS, PR00301; Hsp70; 1
PROSTIE; PS00297; Hsp70; 1.
PROSITE; PS00297; Hsp70_1; 1.
PROSITE; PS00329; Hsp70_2; 1.
ATP-binding; Complete proteome.
SEQUENCE 646 AA; 69759 MW; 2A6IEOB4C74F06C8 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               646 AA
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SEQUENCE 425 AA;
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RESULT 14 AAS11123

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3; Gaps Best Local Similarity 60.0%; Pred. No. 2.7e+02; Matches 12; Conservative 3; Mismatches 2; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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	RESULT 1 US-09-621-976-7555 ; Sequence 7555, Application US/09621976 ; Patent No. 6639063 ; GRNERAL INFORMATION: APPLICANT: Obert, S. TAPLICANT: Obert, S. TITLE OF INVENTION: ESTS and Encoded FILE REFREAMED: SETS and Encoded FILE OF INVENTION UNWER: US/09/621 CURRENT APPLICATION NUMBER: US/09/621 CURRENT FILING DATE: 2000-07-21 ; NUMBER OF SEQ ID NOS: 19335 ; SOFTWARE: Patent.pm ; SEQ ID NO 7555 ; LENGTH: 51 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-621-976-7555	SULT 1  -09-621-976-7555 Sequence 7555, Application US/09621976 Sequence 7555, Application US/09621976 BEEAT NO. 6639063 PREABLI INFORMATION: APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y. TITLE OF INVENTION: ESTS and Encoded Human Proteins FILLE REFERENCE: GENSET. 054PR2 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT PILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: PATENT. PM SOFTWARE: PRICH CONTRACT OF SEQ ID NOS: 19335 LENGTH: 5.1 LENGTH: S.1 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.1 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID NOS: 19355 LENGTH: S.2 CONTRACT OF SEQ ID	-7555 6639063 908MATION: Dumas Milne JODGAT, S. GLOCATION: EST BNCE: GENBET. BNCE: GENBET. ENCATION UM LING DATE: 2 SEQ ID NOS: 1 Patent.pm 1	ation [ ne Edw? S. J.Y. ESTS at ET.054 NUMBLE 1933: 1933:	JS/(1	3, J.B. sncoded 3/09/62:	6 Human 1,976	Protes						
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	දු ය	2 LR 27 LQ	2 LRHWGLQFNTRFG  :            27 LQHWGLHFNMRFG	TRFG 14     MRFG 39	<b></b> 0°									
	RESULT 2 US-09-543-681A-8305 Sequence 8305, Application US/09543681A GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT APPLICATION NUMBER: US 60/128,706 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR FILING DATE: 1999-04-09 SEQ ID NOS: 8344 SEQ ID NO 8305 LENGTH: 149 TYPE: PRT CREATER OF INVENTION NUMBER: US 60/128,706 TRICK FILING DATE: 1999-04-09 SEQ ID NO 8305 LENGTH: 149 TYPE: ORGANISM: Proceus mirabilis US-09-543-681A-8305	SULT 2 Sequence 8305, Application US/09543681A Patent No. 6605709 GENERAL INFORMATION: APPLICANT: GARY BRETON TITLE OF INVENTION: DIAGNOSTICS AND THERA FILE REFERENCE: 2709.1002-001 CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT FILING DATE: 1999-04-05 PRIOR FILING DATE: 1999-04-05 NUMBER OF SEQ ID NOS: 8344 SEQ ID NO 8305 LENGTH: 149 TYPE: PRF ORGANISM: Proteus mirabilis :09-543-681A-8305	4-8305 505070 55, Application U 5605709 GARY BRETON GARY BRETON VENTION: DIAGNO NVENTION: DIAGNO NVENTION: DIAGNO NVENTION: DIAGNO DILCATION NVBER: LING DATE: 1999-04- SEQ ID NOS: 8344 305 Proteus mirabili Proteus mirabili	ation ( ON CON DICTET ONUCLET ONUCLET ONUCLET ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER ONUMBER	15/00 001 001 15/09	0954368 TID AND ICS AND 7/09/54 005	1A AMINO THERA 3,681A 706	ACID &	SEQUENCE	SEQUENCES RELATING		TO PROTEUS	S MIRABILJ	BILLI
<u>.                                    </u>	Query Match	Match		51.2%;	% 	Score 44;		DB 4;	Length 149;	149;				

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1; Mismatches
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US-09-270-767-42163
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-583-110-4596
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 61.5%;
Matches 8; Conservative
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231 LRHWGVTFIGNF 242
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LENGTH: 159
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Sequence 22062, Application US/09252991A

Sequence 22062, Application US/09252991A

Sequence 22062, Application US/09252991A

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PELING DATE: 1998-02-18

PRIOR PELING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22062

LENGTH: 311
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Sequence 20, Application US/09173300

Patent No. 6451581

GENERAL INFORMATION:

APPLICANT: Falco, Saverio Carl

APPLICANT: Hitz, William D.

APPLICANT: Hiney, Anthony J.

APPLICANT: Riney, Anthony J.

APPLICANT: Rafalski, J. Antoni

ITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZY

ITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZY

FILE REFERENCE: B9-1126

CURRENT APPLICATION NUMBER: US/09/173,300

CURRENT FILING DATE: 1998-10-15

EARLIER FILING DATE: 1997 October 28

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Microsoft Word Version 7.0A

SEQ ID NO 20

LENGTH: 363

ITYPE: PRT

COGANISM: Bacillus subtilis

US-09-173-300-20
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  50.0%; Pred. No. 4.8;
                     1; Mismatches
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                                                                 1 TLRHWGLQFNTRFG 14
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Best Local Similarity 63.0
Best Local 7; Conservative
                       7; Conservative
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Matches 7; Conservative
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269 LKHWGLQVSER 279
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Best Local Similarity
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                                                                                                                                                                           RESULT 3
US-09-173-300-20
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                         Matches
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148 LRHWGLQ 154

RESULT 5

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Sequence 4556, Application US/09583110

Fatent No. 6699703

Fatent No. 6699703

GENERAL INFORMATION:
PAPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
CURRENT APPLICATION NUMBER: US/09/583,110

FILE REFERENCE: PATHOG-07A

CURRENT FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

NUMBER OF SEQ ID NOS: 5322

LEMOTH: 265

LEMOTH: 265

LEMOTH: 265

LEMOTH: 265
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENY APPLICATION NUMBER: US/09/540,236
CURRENY ETLING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
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Sequence 42163, Application US/09270767
Patent No. 6703491
Patent No. 6703491
Patent No. 6703491
PILE PRINCENT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE PERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILE DE 111M DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 24;
1; Mismatches 4; Indels
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Pred. No. 29;
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Gaps

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RESULT 10

US-09-248-796A-14319

Sequence 14319, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14319

LENGTH: 737

TANDER DELOTION: TOTAL OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OF
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1 LOCATION: (60)
2 OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknow
US-09-248-7968-14319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Terpstra, Catharinus
APPLICANT: Fol, Johannes M
APPLICANT: Menlenberg, Cabarinus
APPLICANT: Moorman, Robertus J
APPLICANT: Menlenberg, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 46.5%; Score 40; DB 4; Length 737; Best Local Similarity 40.0%; Pred. No. 1.38+02; Matches 6; Conservative 3; Mismatches 6; Indels
                             Score 40; DB 4; Length 674;
Pred. No. 1.2e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,005
FILING DATE: 26-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/08157005; Patent No. 5620691
                                    Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 TIQHWLNNLKTEFGI 369
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                                                                                                                                                                                                                                         54 TGRHWLAAWNSRAGV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Sequence 26476, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT:
MATC J. Rubenfield et al.
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ. ID NO 26476

LENGTH: 674
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Pred. No. 53;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.5%; Score 40; DB 3; Length 674; 53.3%; Pred. No. 1.2e+02; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Augubel, Frederick
APPLICANT: Adodman, Howard M.
APPLICANT: Goodman, Howard M.
APPLICANT: Rahae, Laurence G.
APPLICANT: Tan, Man Wah.
APPLICANT: Tan, Man Wah.
APPLICANT: Tan, Man Wah.
APPLICANT: Tsongalis, John
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE OF INVENTION: 1998-11-25
CURRENT APPLICATION NUMBER: 105/09/199,637A
CURRENT APPLICATION NUMBER: 105/066,517
PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 437
SOSTWARE: FASKESQ FOR WINDOWS VERSION 4.0
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US-09-199-637A-51
; Sequence 51, Application US/09199637A
; Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                            Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                       :: | : | :|||
228 SINEWAMSFQSRFG 241
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54 TGRHWLAAWNSRAGV 68
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Best Local Similarity 53.3%
                                                                 TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-252-991A-26476
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SEQ ID NO 2700
LENGTH: 322
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Gaps

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Gaps

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Sequence 3, Application US/09565864
Sequence 3, Application US/09565864
Patent No. 6455245
GENERAL INFORMATION:
APPLICANT: Wensvoort, Gert
Terpsptra, Catharinus
Pol, Johannes M
Moorman, Robertus J
Mellenberg, Johanna J
CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
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Pred. No. 2.7e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
COUNTRY: USA
ZIP: 1012
COMPUTER: New York
COUNTRY: USA
ZIP: 10112
COMPUTER: EDAPPO disk
COMPUTER: EDAPPO disk
COMPUTER: EDAPPO disk
COMPUTER: EDAPPO disk
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COMPUTER: EDAPPO disk
APPLICATION NUMBER: US/09/565,864
FILING DATE: OBANDA DATE:
APPLICATION NUMBER: EP 91201398.4
FILING DATE: OBANDA DATE: BP 91201398.4
FILING DATE: OBANDA DATE: DAPPLICATION NUMBER: EP 92200781.0
FILING DATE: OBANDA DATE: OBANDA DAPPLICATION NUMBER: EP 92200781.0
RILING DATE: OBANDA DATE: OBANDA DAPPLICATION NUMBER: EP 92200781.0
RILING DATE: OBANDA DATE: OBANDA DAPPLICATION NUMBER: EP 92200781.0
REGISTRATION NUMBER: 16,579
REGISTRATION NUMBER: 16,579
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
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TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
         PRIOR APPLICATION DATA:

APPLICATION UNBER:
FILING DATE: 05-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: TUTNET, Allan C.
REGISTRATION NUMBER: 33041
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 532-1922
TELEFRX: (801) 531-9168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1463 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RHWGLOFNTRFG 14
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; Sequence 3, Application US/08747863
; Patent No. 6197310
; GENERAL INFORMATION:
    APPLICANT: Wensyoort, Gert
    APPLICANT: Pol, Johannes M
    APPLICANT: Moorman, Robertus J
    APPLICANT: Meulenberg, Johanne J
    TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
    TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Trask, Britt & Rosea
    STREET: S.25 South, 300 East
    CITY: Salt Lake City
    STATE: Utah
    COUNTRY: USA
    ZIP. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 4; Indels
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

# APPLICATION NAWBER: EP 51201398.4

FILING DATE: 06-JUN-1991

PRIOR APPLICATION NUMBER: EP 92200781.0

# APPLICATION NUMBER: EP 92200781.0

FILING DATE: 18-MAR-1992

PRIOR APPLICATION NUMBER: PCT NL92/00096

# APPLICATION NUMBER: PCT NL92/00096

# ATTORNEY/AGENT INFORMATION:

NAME: Noran, Thomas F

REGISTRATION NUMBER: 44819

TELECOMMUNICATION NUMBER: 44819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/157,005
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92200781.0
FILING DATE: ,18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 84111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RHWGLQFNTRFG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-157-005-3
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Search completed: November 10, 2004, 15:57:25 Job time: 7.9395 secs
        298 WRQQFKARFGV 308
        엄
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4527, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY REFORM
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR FILING DATE: 1999-04-09

NUMBER: OS EQ ID NOS: 8344

SEQ ID NO 4527

LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
FILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10546
LENGTH: 321
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                                                                                                                                                                                          Length 1463;
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Pred. No. 66;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 4; Length 321; Pred. No. 77; 0; Mismatches 4; Indels
                                                                                                                                                                                      Query Match
46.5%; Score 40; DB 4; Length 146
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 4; Indels
                                                                       RESULT 15
US-009-489-039A-10546
Sequence 10546, Application US/09489039A
Patent No. 6610836
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Proteus mirabilis US-09-543-681A-4527
                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                156 RHKGRLINTRFG 167
                                                                                                                                                                                                                                                                      3 RHWGLOFNTRFG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 LSHWG--FNTR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LRHWGLQFNTR 12
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US-09-543-681A-4527
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RESULT 2
US-10-106-698-5549
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Sequence 5549, Ap
Sequence 48915, A
Sequence 27075,
Sequence 27075,
Sequence 410, App
Sequence 410, App
Sequence 410, App
Sequence 201421,
Sequence 25198,
Sequence 8569, Ap
                                                                                                                          November 11, 2004, 02:43:24; Search time 36.2456 Seconds (without alignments) 146.426 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-10-106-698-5549
US-10-282-115-148915
US-10-425-115-187835
US-10-424-599-267075
US-10-424-599-267075
US-10-424-599-267075
US-10-253-410
US-10-253-410
US-10-253-410
US-10-425-115-201421
US-10-425-115-317138
US-10-156-761-893
                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                1568699 seqs, 353819137 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
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Maximum DB seq length: 2000000000
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86
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sequence 267, App
Sequence 125343,
Sequence 125343,
Sequence 58855, A
Sequence 358150,
Sequence 358150,
Sequence 36811,
Sequence 101149,
Sequence 101149,
Sequence 3062, Ap
Sequence 31, App
Sequence 31, App
Sequence 13770, A
Sequence 13507, A
Sequence 12507, A
Sequence 26918,
Sequence 26918,
Sequence 26918,
Sequence 34, Appl
Sequence 26918,
Sequence 26918,
Sequence 34, Appl
Sequence 26918,
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
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Sequence 13891, A
                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
6 US-10-437-963-136940

US-09-314-879-279

US-09-316-736-267

US-09-818-683-267

US-09-818-683-267

US-09-818-683-267

US-10-421-401-273

5 US-10-421-114-58855

5 US-10-425-114-58855

5 US-10-425-114-58855

7 US-10-425-114-58855

7 US-10-425-114-58855

8 US-10-425-114-70483

4 US-10-369-433-5480

US-10-425-114-70483

6 US-10-425-114-70483

6 US-10-425-115-35151

US-09-908-11-81

US-09-908-11-81

US-09-164-31-962

US-09-164-31-962

US-09-164-31-962

US-09-164-31-962

US-09-164-31-962

US-09-164-31-962

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US-09-164-31-962

US-10-474-776-314

4 US-10-282-122A-64833

US-10-282-122A-64833

US-10-424-599-143368

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### ALIGNMENTS

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Gaps
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Sequence 228, Application US/10092750
| Bublication No. US2003003157A1
| GENERAL INFORMATION, Philip W. |
| APPLICANT: Harmond, Philip W. |
| APPLICANT: Harmond, Philip W. |
| APPLICANT: Alpin, Julia |
| TILE OF INVENTION: Polypeptides Interactive with BCL-XI |
| TILE OF INVENTION: Polypeptides Interactive with BCL-XI |
| FILE REFERENCE: 50036/050002 |
| CURRENT PILING DATE: 2002-03-07 |
| PRIOR PILING DATE: 2001-03-08 |
| NUMBER OF SEQ ID NOS: 253 |
| SOFTWARE: EastSEQ for Windows Version 4.0 |
| SEQ ID NO 228 |
| LENGTH: 15 |
| TYPE: PRT |
| ORGANISM: Homo sapiens |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 15; Conservative
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# 1 TLRHWGLQFNTRFGV 15

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Sequence 5549, Application US/10106698 Publication No. US20030109690A1 GENERAL INFORMATION:

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Sequence 26705, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: APOLICANT: Tak Rosa Thomas J

APPLICANT: Cao Yongwei

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 2003-04-28

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

ENDIRER OF SEQ ID NOS: 285684

ENDIRER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Everalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con Yongwan
TITLE OF INVENTION: Nacleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 187832
LENGTH: 71
                                                                                                                                                    Query Match
Best Local Similarity 72.7%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 17; Length 71;
Pred. No. 18;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8318C.1.pep
US-10-424-599-267075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: MRT4577_102889C.1.pep
US-10-425-115-187832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-10-425-115-187832
Sequence 187832. Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                         TYPE: PRT ORGANISM: Bacteroides fragilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.2%;
50.0%;
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Best Local Similarity 50.v
                                                                                                                                                                                                                                                                                                                                                                  208 WNLNLNTRFGV 218
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8 MRHWTLEYGTRW 19
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ORGANISM: Zea mays
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US-10-424-599-267075
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR PILING DATE: 2000-09-29
PRIOR PLING DATE: 1999-09-29
PRIOR PLING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTHAME: Patentin Ver: 3.0
SEQ ID NO 5549
LENGTH: 113
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REPERENCE: ELITRA.034A

CURRENT PELLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/257, 931

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

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PRIOR PLING DATE: 2001-02-06

PRIOR PRIOR DATE: 2001-02-06

PRIOR PRIOR DATE: 2001-02-06

PRIOR PRIOR DATE: 2001-02-06

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Pred. No. 0.75;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyekind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 76.9%;
Matches 10; Conservative
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USCALLAND APPLICATION US/10253471

Sequence 410, Application US/10253471

Publication No. US20030236190A1

GENERAL INFORMATION: US20030236190A1

APPLICANT: PILLUTLA, RENUKA et al.

TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS

FILE REFREENCE: 1879-4057

CURRENT APPLICATION NUMBER: US/10/253,471

CURRENT PILING DATE: 2002-09-24

PRIOR APPLICATION NUMBER: 09/538,038

PRIOR PILING DATE: 2000-09-24

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1998-09-02

NUMBER OF SEQ ID NOS: 2227

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 410

LENGTH: 26
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Sequence 410. Application US/10253493

Publication No. US20040023887A1

SEQUENCE 410.

Publication No. US20040023887A1

SEQUENCE TO FILEUTHA, RENUEN & et al.

TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS

TITLE OF INVENTION: 1878-4056

CURRENT APPLICATION NUMBER: US/10/253,493

CURRENT APPLICATION NUMBER: 09/962,756

PRIOR PILING DATE: 2001-09-24

PRIOR FILING DATE: 2001-03-29

PRIOR PILING DATE: 1908-09-24

PRIOR PILING DATE: 1908-09-02

NUMBER OF SEQ ID NOS: 2227

SOFTO D NO 410

LENGTH: 26

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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-10-253-493-410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-10-253-471-410
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Mismatches
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ORGANISM: Artificial Sequence
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Matches 7; Conservative
  7; Conservative
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1 RNWNLOFNENF 11
                                                3 RHWGLQFNTRF 13
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     Matches
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APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTAN: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
TITLE OF INVENTAN: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
CURRENT APPLICATION NUMBER: US/10/027,450
CURRENT APPLICATION NUMBER: 001-12-20
PRIOR APPLICATION NUMBER: 00063,423
PRIOR PLING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
LENGTH: 363
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APPLICANT: BLUME, ARTHUR J.
APPLICANT: BLUME, ARTHUR J.
APPLICANT: BLUME, ARTHUR J.
APPLICANT: BLUME, ARTHUR J.
APPLICANT: SCHAFFER, LAUGE
APPLICANT: GOLDSTEIN, JAKOB
APPLICANT: GOLDSTEIN, WILL I.
APPLICANT: SPETZLER, JANE
APPLICANT: SPETZLER, JANE
APPLICANT: OSTERCAARD, SOREN
APPLICANT: OSTERCAARD, SOREN
APPLICANT: OSTERCAARD, SOREN
APPLICANT: OSTERCAARD, SOREN
APPLICANT: NUMBER: US/09/962,756
CURRENT APPLICATION NUMBER: US/09/962,756
CURRENT APPLICATION NUMBER: 09/538,038
PRIOR APPLICATION NUMBER: 09/538,038
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 2227
SOFTWARE: PALCHIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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87;
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Pred. No. 9.9;
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Pred. No.
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Publication No. US20030195147A1
                                                                                                                                                                   Sequence 20, Application US/10027450 Publication No. US20020102715A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: Bacillus subtilis
US-10-027-450-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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269 LKHWGLQVSER 279
       LRHWGLOFNTRF 13
                                                     16 LLHWGVLFNSTF 27
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Best Local Similarity
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GENERAL INFORMATION:
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LENGTH: 26
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Query Match 50.0%; Score 43; DB 14; Length 308; Best Local Similarity 54.5%; Pred. No. 1.1e+02; Matches 6; Conservative 2; Mismatches 3; Indels
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                                           APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIKAWA, UUN
APPLICANT: SHIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, WOSHITWI
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-222
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
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PRIOR PILING DATE: 2001-05-30
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Fublication No. US20030119018A1
GERREAL INFORMATION
JEDELICANT: OWURA, SATOSHI
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, UNN
APPLICANT: SHIKAWA, UNN
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, WASHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
FRIOR FILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-06-02
NUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 14693
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Streptomyces avermitilis US-10-156-761-8569
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US-10-156-761-14693
Publication No. US20030119018A1
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Best Local Similarity 88.9
Matches 8; Conservative
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US-10-437-963-136940
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                                                                                                                                                                             Sequence 201421, Application US/10425115
; Sequence 201421, Application US/10425115
; bublication No. US20040214272A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Vadic, David K.
    APPLICANT: Cao, Yongwei
    APPLICANT: Cao, Yongwei
    APPLICANT: ANGLAIC Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants
    FILLE REFRENCE: 38 22 (5222)8
    FILLE REPRENCE: 38 22 (5222)8
    CURRENT APPLICATION NUMBER: US/10/425,115
    CURRENT PILING DATE: 2003-04-28
    NUMBER OF SEQ ID NOS: 369326
    SEQ ID NO 201421
    LENGTH: 85
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Sequence 357198, Application US/10425115

Sequence 357198, Application US/2040214272A1

Sequence 357198, Application US/2040214272A1

Sequence 357198, Application US/2040214272A1

APPLICANT: La Rosa, Thomas J.

APPLICANT: Takou, Yihuas J.

APPLICANT: Cakou, Yongwei

APPLICANT: Cakou, Yongwei

TITLE OF INVENTION: Plants

FILLE REPRENCE: 38-21(5322)B

CURRENT APPLICANT: 2003-04-28

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 357198

LENGTH: 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%; Score 43; DB 17; Length 85; 77.8%; Pred. No. 31; 17.8%; Live 1; Mismatches 1; Indels
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US-10-425-115-201421
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US-10-425-115-357198
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US-10-156-761-8569
(1) Sequence 8569, Application US/10156761
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 6, Conservative
                            3 RHWGLOFNTRF 13
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1 RNWNLQFNENF 11
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77 LRKWGLEFN 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays
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Sequence 136940, Application US/10437963 Publication No. US20040123343A1

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Pred. No. 52;
2; Mismatches 5; Indels
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Job time : 36.2456 secs
     PRIOR FILING DATE: 1997-11-17

PRIOR APPLICATION NUMBER: US 60/066,095

PRIOR FILING DATE: 1997-11-17

PRIOR PILING DATE: 1997-11-17

NUMBER OF SEQ ID NOS: 611

SEQ ID NO 279

LENGTH: 100
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Best Local Similarity 50.0%;
Matches 7; Conservative
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58 SLRSWGAKLGLRFG 71
                                                                                                                                                                                                                                  t TYPE: PRT
CORGANISM: Homo sapiens
US-09-974-879-279
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APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TILLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (52221) B

CURRENT APPLICANTON NUMBER: US/10/437,963

NUMBER OF SEQ ID NOS: 204966

LENGTH: 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_38471C.1.pep
US-10-437-963-136940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-974-879-279
Sequence 279, Application US/09974879
Sequence 279, Application US/09974879
Sequence 279, Application US/09974879
FULD CENERAL INFORMATION:
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P2
CURRENT APPLICATION NUMBER: US/09/974,879
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/818,683
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 09/818,683
PRIOR APPLICATION NUMBER: US 09/305,736
PRIOR APPLICATION NUMBER: US 09/305,736
PRIOR PILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: US 60/064,912
PRIOR APPLICATION NUMBER: US 60/064,912
PRIOR PILING DATE: 1998-11-07
PRIOR PILING DATE: 1997-11-07
PRIOR PILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,987
PRIOR PILING DATE: 1997-11-07
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PRIOR PILING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LRHWGLOFNTRFGV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | || :|| :
28 LHHWAMQFKEHFTI 41
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                    Copyright
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32; Search time 5.79275 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

US-10-092-750-31 Title: Perfect score:

143 1 MRDLPGHYYETLKFLVGHLKTIADHR 26 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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cion	٠.	4 prot	protein	PTPL1-associated	hypothetical	tical	rin -	bud emergence	4 prote	beta-chimerin	beta2-chimerin,	beta2-chimerin,	hypothetical	hypothetical	rin h	ŭ	rin -		ase a	hypothetical	redu	tical	tical	tical	ed hy	tical	e glute	hatid	e gluti
Description	വ	N	ZC21.4 1	L1-a8	other	hypothetica	N-chimerin	eme	KIAA1204	a-ch:	a2-c)	a2-c1	othe	other	N-chimerin	hypotheti	N-chimerin	N-chimerin	GTPase	othe	nitrate	hypothetica	hypothetica	hypothetic	serve	other	probable	hospl	probable gl
Des	KIN	KIAA1	ZCZ	PTF	hyp	hyp	N-N	pnq	KIA	bet	bet	bet	hyr	hyr	Z	hyr	N-N	,	Rho	hyp	nit	hyr	hyr	1 Tr	COL	hyg	pro	3-p	pro
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DB	7	~	7	~	~	N	7	7	7	N	N	7	7	N	0	0	0	N	N	Ŋ	N	N	(1	N	N	N	7	N	N
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% Query Match		64	46	45	44	44	42	40	39	38	38	38	38	38	38	38	37	37	37	35	35	35	34	34	34		33	33	33
Score	13	92	67	65	64	64	61	28	26	55	55	55	55	55	55	55	54	54	53	51	51	20	4,	<b>4</b> ,	4.	<b>4</b>	48	48	48
Result No.	-	7	m	4	Z.	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

ASTALA1424 protein [imported] - human Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Jun-2002 #sequence_revision 03-Jun-2002 #sequence_revision 03-Jun-2002 #sequence_revision 05-Jun-2002 #sequence cispecies: Tiskinno, R.; Ishikawa, K.I.; Hirosawa, M.; Ohara, O. DNA Res. 7, 65-73, 2000 coding sequences of unidentified human genes. XVI. The complet A; Reference number: A59438 A; Accession: A59438 A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; Molecule type: MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A; MRNA A;

C. elegans protein	transmembrane prot	alpha,alpha-trehal	hypothetical prote	Gem-interacting pr	hypothetical prote	probable membrane	hypothetical prote	hypothetical prote	thyroid stimulatin	aspartate kinase (	98K GTPase-activat	chromosome 5 GAP-1	GP80 precursor - s	conserved hypothet	transcription fact
D59433	S42612	S36868	AE1169	D59435	B86241	S19427	T40031	T22329	JC5643	AH0056 .	A49307	B59433	T31344	D72396	833223
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1165	2437	1098	326	970	1358	953	290	718	764	819	859	915	1289	150	331
33.6	33.6	33.2	32.9	32.9	32.9	32.5	32.2	32.2	32.2	32.2	32.2	32.2	32.2	31.5	31.5
48	48	47.5	47	47	47	46.5	46	46	46	46	4.6	46	46	45	<b>4</b> 4.
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## ALIGNMENTS

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ACTAINS protein [imported] - human C.Species: Homo sapiens [man]
C.Species: Homo sapiens [man]
C.Species: Homo sapiens [man]
C.Species: Homo sapiens [man]
C.Species: Homo sapiens [man]
C.Species: Homo sapiens [man]
C.Species: Homo sapiens [man]
C.Species: Homo sapiens [man]
R.Nagase, T.; Kikuno, R.; Ishikawa, K.; Hirosawa, M.; Ohara, O.
mRNA Res. 7, 143-150, 2000
A.Title: Prediction of the coding sequences of unidentified human genes. XVII. The complé
A.Reference number: A59434
A.Status: Prediction A59434
A.Status: Prediminary
A.Status: Prediminary
A.Status: Prediminary
A.Status: Prediminary
A.Status: R.Shara, O.; Nagase, T.; Kikuno, R.
R.Shara, O.; Nagase, T.; Kikuno, R.
R.Shara, O.; Nagase, T.; Kikuno, R.
A.Steference number: B59434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-735 <-GNA>
A;Cxos-references: GB:BAA96025; PID:g7959263; PIDN:BAA96025.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRDLPGHYYETLKFLVGHLKTIADH 25
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Gaps

Length 1944;

Query Match 64.3%; Score 92; DB 2; I Best Local Similarity 64.0%; Pred. No. 6.3e-05; Matches 16; Conservative 5; Mismatches 4

1249 IHDLPEHHYETLKFLSAHLKTVAEN 1273

RESULT 3

1 MRDLPGHYYETLKFLVGHLKTIADH 25

A;Status: preliminary A;NoLecule type: mRNA A;Residues: 1-1944 (-0HA> A;Cross-references: GB:BAA92662; PID:g20521912; PIDN:BAA92662.2

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                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-634 «MI2)
A;Coss-references: EMBL:246812; PIDN:CAA86848.1; GSPDB:GN00020; CESP:ZK669.1b
A;Experimental source: clone ZK675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:246812; PIDN:CAA86847.1; GSPDB:GN00020; CESP:ZK669.1a
A;Experimental source: clone ZK675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ZK669.1a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27958; T27973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 2
A:Introns: 9/3; 57/2; 158/3; 211/3; 325/2; 474/1; 524/1; 551/3; 563/1
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ilarity 54.5%; Pred. No. 0.33;
Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: T27958
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A,Molecule type: DNA
submitted to the EMBL Data Library, September 1994
A;Reference number: 220446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Thomas, K.
submitted to the EMBL Data Library, September 1994
A:Reference number: Z20446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, November 1994 A;Reference number: Z20448 A;Accession: T27973
                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November 1994 A;Reference number: Z20448 A;Accession: T27974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-chimerin - rat
N;Alternate names: GTPase-activating protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 RKLPVHNYETLKFIMLHLNRVS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 RKLPVHNYETLKFIMLHLNRVS 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RDLPGHYYETLKFLVGHLKTIA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: clone ZK669
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-863 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: ZK669.1b
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                                                                A; Accession: T27959
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R;Saras, J.; Franzen, P.; Aspenstrom, P.; Hellman, U.; Gonez, L.J.; Heldin, C.-H. Submitted to GenBank, December 1997
A;Description: Homo sapiens PTPL1-associated KhoGAP 1 (PARG1), mRNA.
A;Reference number: ES9430
A;Accession: ES9430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-1261 <5R>
A,Cross-references: UNIPROT:O15463; GB:NP_004806; PID:g4758882; PIDN:NP_004806.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ZC21.4 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C;Accession: S44876
B;Du, Z.; Waterston, R.
Submitted to the EMBL Data Library, May 1993
A;Reference number: S44649
A;Reference number: S44649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ZK669.1b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T27959; T27974
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Gaps

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Query Match
46.9%; Score 67; DB 2; Length 733;
Best Local Similarity 48.0%; Pred. No. 0.1;
Matches 12; Conservative 5; Mismatches 8; Indels

1 MRDLPGHYYETLKFLVGHLKTIADH 25

A;cross-references: EMBL:L16685; NID:g289729; PID:g289735 C;Genetics:

A Status: preliminary A Molecule type: DNA A Residues: 1-733 < DUZ>

A; Introns: 269/3; 551/3; 600/2; 670/3

PTPL1-associated RhoGAP protein 1 [imported] - human C;Species: Homo sapiens (man) C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004

Gaps

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/ Match 45.5%; Score 65; DB 2; Length 1261; Local Similarity 44.0%; Pred. No. 0.35; noservative 5; Mismatches 9; Indels

Best Loca Matches

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:| || : :| || : || 807 LRQLPASNFNSLHFLIVHLKRVVDH 831

1 MRDLPGHYYETLKFLVGHLKTIADH 25

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A)Status: preliminary, translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Nosidues: 1-634 GMIL-
A;Residues: 1-634 GMIL-
A;Cross-references: UNIRROT:07YSI8; EMBL:237093; PIDN:CAA85469.1; GSPDB:GN00020; CESP:ZKK
A;Experimental source: clone ZK669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1.863 <WIL>
A;Cross-references: UNIPROT:Q27267; EMBL:Z37093; PIDN:CAA85468.1; GSPDB:GN00020; CESP:ZKf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 2
A;Introns: 62/3; 125/3; 185/3; 211/3; 238/3; 286/2; 387/3; 440/3; 554/2; 703/1; 753/1;
```

25

1 MRDLPGHYYETLKFLVGHLKTIADH

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KIAA1204 protein [imported] - human G.Species: Homo sapiens (man) G.Species: Homo sapiens (man) C.Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004 C.Accession: A59437; B59437; B59437; B7,Nagase, T.; Ishikawa, K.; Kikuno, R.; Hirosawa, M.; Nomura, N.; Ohara, O. DNA Res. 6, 337-345, 1999 A.Title: Prediction of the coding sequences of unidentified human genes. XV. The complete A,Reference number: A59437
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NiAlternate names: GTPase-activating protein

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (S2956

R;Leung, T.; How, B.E.; Manser, E.; Lim, L.

J. Biol. Chem. 268, 3813-3816, 1993

A;Title: Germ cell beta-chimaerin, a new GTPase-activating protein for p21rac, is specifit A;Reference number: A454885; MUID:93179371; PMID:8440677
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A/Status: prefininary
A/Status: prefininary
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Cross-references: UNIPROT:Q03070; EMBL:X69489; NID:g57526; PIDN:CAA49244.1; PID:g57527
A/Cross-references: UNIPROT:Q03070; EMBL:X69489; NID:g57526; PIDN:CAA49244.1; PID:g57527
A/Mole: sequence extracted from NCBI backbone (NCBIP:125731)
B/Leurg; T.; How, B.B.; Manser, E.; Lim, L.
A/Molecula (T.) How, B.B.; Manser, E.; Lim, L.
A/Molecula (T.) And Library, November 1992
A/Molecula (T.) A/Molecula Library, November 1992
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A/Molecula (T.) A/M
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F;42-91/Domain: protein kinase C zinc-binding repeat homology <KZ2>
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A;Molecule type: mRNA
A;Residues: 1-1445 <OHA>
A;Cross-references: GB:BAA86518; PID:g6382020; PIDN:BAA86518.1
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Pred. No. 2.2;
5; Mismatches
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Pred. No. 8.3;
7; Mismatches
                                                                                    2090 LQKLPTCYYQTLKRIVFHLNKVHQH 2114
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Afstatus: preliminary
Afmoleule type: mRNA
Afcesidues: 1-1445 «NMG»
Afcross-references: UNIPROT:QUULL6; GB
Ribhara, O.; Nagase, T.; Kikuno, R.
submitted to GenBank, October 1999
Afreference number: B59437
Afacession: B59437
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Best Local Similarity 43.5%;
Matches 10; Conservative
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Best Local Similarity 52.6
Matches 10; Conservative
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A,Residues: 1-295 <LE2>
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C;Species: Rattus norvegicus (Norway rat)
C;Jate: 25-Reb-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S29128; S25152
B;Lim, H.H.; Michael, G.J.; Smith, P.; Lim, L.; Hall, C.
B;Lim, H.H.; Michael, G.J.; Smith, P.; Lim, L.; Hall, C.
B;Cochem, J. 287, 415-422, 1992
B;Title: Developmental regulation and neuronal expression of the mRNA of rat n-chimaerin A;Reference number: S29128; MUID:93074974; PMID:1445199
B;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Residues: 1-334 <LIM>
A)Residues: 1-334 <LIM>
A)Cross-references: UNIPROT: P30337; EMBL: X67250; NID: 955939; PIDN: CAA47672.1; PID: 955946
R)Lim, H.; Michael, G.J.; Smith, P.; Lim, L.; Hall, C.
Submitted to the EMBL Data Library, July 1992
A)Description: Rat n-chimaerin a p21rac GAP: CDNA sequence developmental regulation and n
A)Reference number: S25152
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SSO658

Shod emergence protein BEM2 - yeast (Saccharomyces cerevisiae)

N.Alternate names: GTPase-activating protein IPL2; protein YER155c
C;Species: Saccharomyces cerevisiae
C;Date: 28-Jan-1995 #sequence revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S50658; AS5155; Ā55156
R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 8229, 9115, 9132, 9981, and lambda
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A;Molecule type: DNA
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A; Residues: 1-2167 (XIM)
A; Cross-references: (B:Z35159; NID:9511136; PIDN:CAA84524.1; PID:9511137
A; Cross-references: (B:Z35159; NID:9511136; PIDN:CAA84524.1; PID:9511137
B; Peterson, J.; Zheng, Y.; Bender, L.; Myers, A.; Cerione, R.; Bender, A.
C. Call Biol. 127, 1355-1406, 1594
A; Tille: Interactions between the bud emergence proteins Bemip and Bemzp and Rho-type
A; Reference number: A55156; MUID:95050997; PMID:7962098
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;Residues: 1-2167 <PET>
;Cross-references: GB:L33832; NID:g499694; PIDN:AAA57132.1; PID:g499695
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Best Local Similarity 44.0%; Pred. No. 0.33;
Matches 11; Conservative 6; Mismatches
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Cross-references: SGD:S0000957; MIPS:YER155c
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Best Local Similarity 44.0%;
Matches 11; Conservative
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A/Status: preliminary, translated from GB/EMBL/DDBJ
A/Status: preliminary, translated from GB/EMBL/DDBJ
A/Status: 1-903 cLAM>
A/Residues: 1-903 cLAM>
A/Cross-references: UNIPROT:014560, EMBL:AC002398; NID:g2529398; PIDN:AAB81198.1, PID:g26.96enetics:
A/Map position: 19
A/Map position: 19
A/Introns: 17/3; 68/3; 100/2; 148/3; 176/2; 212/2; 261/1; 312/2; 36i/1; 513/1
A/Note: F25965_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T00705
R;Lamerdin, J.E.; McCready, P.M.; Adamson, A.W.; Burkhart-Schultz, K.; Garcia, E.; Kyle, hi, A.; Olsen, A.O.; Carrano, A.V.
submitted to the EMBL Data Library, October 1997
A;Description: Sequence analysis of a 1Mb region in 19q13.1.
A;Reference number: Z14199
A;Accession: T00705
                                                 A;Map position: 3
A;Introns: 31/3; 81/2; 137/3; 277/2; 435/3; 507/3; 544/2; 604/1; 646/2; 707/1; 791/3
F;96-133/Domain: WW repeat homology <WWR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-chimerin homolog F25965_3 - human
C,Species: Homo sapiens (man)
C,Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein DKFZp434A1010.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. Bibmitted to the Protein Sequence Database, January 2000
A;Reference number: 233035
A;Accession: T46289
A;Accession: preliminary
A;Accession: Breliminary
A;Retectual type: mRNA
A;Residues: 1-862 < AAA>
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                                                                                                                                                     DB 2; Length 837;
6.5;
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A;Experimental source: adult testis; clone DKF2p434A1010
C;Genetics:
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Pred. No. 7.1;
7; Mismatches
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                                                                                                                                                       Query Match 38.5%; Score 55; DB Best Local Similarity 50.0%; Pred. No. 6.5; Matches 11; Conservative 2; Mismatches
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38.5%; Score 55;
Best Local Similarity 40.0%; Pred. No.
Matches 10; Conservative 7; Mismatc
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IQQLPPPHYRTLEYLLRHLARMARH 191
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Best Local Similarity 40.09
Matches 10; Conservative
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                          A; Gene: CESP: C38D4.5
C; Genetics:
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A;Cross-references: UNIPROT:P46941; EMBL:Z46241; PIDN:CAA86318.1; GSPDB:GN0021; CESP:C3
A;Experimental source: clone C38D4
                                                                                                                                                          N/Alternate names: GTPase-activating protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 04-Apr-2004
C;Accession: B53764 B.E.; Manser, E.; Lim, L.
R;Leung, T.; How, B.E.; Manser, E.; Lim, L.
J. B;Ol. Chem. 269, 12888-12892, 1994
A;Title: Cerebellar beta2-chimaerin, a GTPase-activating protein for p21 Ras-related Rac
A;Reference number: A53764; MUID:94230370; PMID:8175705
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A;Residues: 1-466 <LEU>
A;Cross-references: UNIPROT:P52757; GB:L29126; NID:g457229; PIDN:AAA19191.1; PID:g457236
F;57-137/Domain: SH2 homology <SH2>
F;27-137/Domain: protein Kinase C zinc-binding repeat homology <K22>
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R.Ibeung, T.: How, B.E.: Manser, E.; Lim, L.
J. Biol. Chem. 269, 12988-12892, 1994
J. Biol. Chem. 269, 12988-12892, 1994
J. Biol. Chem. 269, 12988-12891
J. Biol. Chem. 269, 12988-12891
J. Biol. Chem. 269, 12988-12892, 1994
J. Ras-related J. A.; Reference number: A53764; MUID:94230370; PMID:8175705
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C;Species: Caenorhabditis elegans
C;Datte: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19825
R;Coles, L.
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NALlerante names: GTRese-activating protein
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
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F;190-239/Domain: protein kinase C zinc-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-443 <LEU>
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38.5%; Score 55; DB 2; Length 443;
Best Local Similarity 52.6%; Pred. No. 3.3;
Matches 10; Conservative 5; Mismatches 4; Indels
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A;Molecule type: DNA.
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LPPAHYETLRYLMIHLKKV 411
        222 LPPAHYETLRYLMIHLKKV 240
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nes 10; Conserv
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                                                                                          RESULT
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Job time : 6.79275 secs

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homo sapien caenorhabdi homo sapien

Q80xd1 P52757 P46941 Q9nt23

735 AA

ALIGNMENTS

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MEDINE=20277482; PubMed=10819331;

MEDLINE=20277482; PubMed=10819331;

MEDLINE=20277482; PubMed=10819331;

MEDLINE=20277482; PubMed=10819331;

MEDLINE=20277482; PubMed=10819331;

MEDLINE=20277482; PubMed=10819331;

The complete sequences of unidentified human genes. XVII.

The complete sequences of 100 new cDNA clones from brain which code if in the complete sequences of 100 new cDNA clones from brain which code in the complete sequences of 100 new cDNA clones from brain which code in the complete sequences of 100 new cDNA clones from brain which code in the protection in the complete sequences of 100 new cDNA clones from brain which code in the complete sequences in the complete sequences in the complete sequences in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code in the code i
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 1.2e-10;
1; Mismatches 0;
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                       06P4P5
AAH63321
A9ULL6
C9VLS1
C9VRS7
C75MRS7
C75MRS7
C75MRS7
C8D9W82
CHIO RAT
C80ND1
CHIO RAT
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VIEE CAEEL
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01-0CT-2004 (TrEMBLrel. 28, Last seq
01-0CT-2004 (TrEMBLrel. 28, Last ann
Hypothetical protein.
Xenopus laevis (African clawed frog)
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Best Local Similarity 96.0%;
Matches 24; Conservative
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Name=KIAA1501;
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817
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1843
1843
263
276
276
276
282
295
332
837
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NON TER
SEQUENCE
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Q9P227
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Q6DFG0
ID Q6DFG
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Q80gf1 mus musculu
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Q77818 caenorhabdi
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Q60cs4 brachydanio
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WEDLINE=2288257; PubMed=12477932;

WEDLINE=2288257; PubMed=12477932;

RIGUINE=2288257; PubMed=12477932;

Rapleton M., Soares M.B., Boneldo M.F., Canadon C.M., Scheezz T.E., Rapleton M.J., Moders C.J., Abramson R.D., Mullahy S.J., Rochezt G.J., Abramson R.D., Mullahy S.J., Richards S.M., Moden P.J., McKernan K.J., Malek J.M., Ganezatne P.H., Raha S.S., Worltenan M., Sacria A.M., Gabbs R.A., Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Milting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G., Milting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S., R. Todriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S., R. Todriguez A.C., Marra M.A., Schmerch A., Schmer
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKF2p761J031 (Fragment).
Name-DKF2p761J031;
Mame-DKF2p761J031;
Buhearyota, Mctazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Ottenwaelder B., Obermaier B., Mewes H.W., Weil B., Wiemann S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC077778; AAT6778.1; -.
Hypothetical protein.
SEQUENCE 1926 AA; 214711 MW; FA7FCCF57681DD32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                  NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                 64.3%; Score 92; DB 2; Length 1321;
64.0%; Pred. No. 0.00027;
ive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                           NON TER 1
SEQUENCE 1321 AA; 146862 MW; A190E9B171EBF015 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1902 AA.
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-!- SIMILARITY: Contains 1 PDZ/DHR domain.
EMBL, AR62392, AAG04821.1; -.
INTERPRO; IPR001478; PDZ.
INTERPRO; IPR001478; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRDLPGHYYETLKFLVGHLKTIADH 25
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InterPro; IFFOCIATION FH related.
InterPro; IFFOCIATION FH related.
InterPro; IFFOCO198; RhoGAP.
InterPro; IFFOCO169; RhoGAP.
InterPro; IFFOCO1605; Spectrin_PH.
Ffam; PFOCO609; PH; 1.
Pfam; PFOCO609; RhoGAP; 1.
PART; SMOC203; PH; 11.
SWART; SMOC324; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO11036; PH related.
InterPro; IPRO0199; RhGGAP.
Pfam; PP00595; PDZ; 1.
Ffam; PP00169; PH; 1.
Ffam; PP00169; PH; 1.
Ffam; PP000169; PH; 1.
SWART; SM00228; PH; 1.
SWART; SM00228; PH; 1.
SWART; SM00239; PH; 1.
FROSITE; PS50106; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
PROSITE; PS50038; RHGGAP; 1.
PROSITE; PS50038; RHGGAP; 1.
SROSITE; PS50038; RHGGAP; 1.
SROSITE; PS50038; RHGGAP; 1.
SROSITE; PS50038; RHGGAP; 1.
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                                                                                                                                                                                                                                             PROSITE; PS50003; PH DOMAIN; 1. PROSITE; PS50238; RHÖGAP; 1. Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 64.0%;
Matches 16; Conservative
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NON TER 1 1
SEQUENCE 1944 AA; 215996 WW, 1FDC44670235487F CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
MXIAA1424 protein (Fragment).
Name=Arhgap21; Synonyms=mKIAA1424;
                                                                                                             Query Match
Best Local Similarity 64.0%;
Matches 16; Conservative
PROSITE; PS50238; RHOGAP; 1.
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SMART; SM00233; PH; 1.
SMART; SM00324; RhoGAP; 1.
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Best Local Similarity
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Q8N119
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0807D7
ID 0807I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22997565; PubMed=12711552; Kim U., Shim S., Choi S.C., Han J.K.; Man J.K.; Shim S., Choi S.C., Han J.K.; A publative Xenopus Rho-Grpase activating protein (XrGAP) gene is expressed in the notochord and brain during the early embryogenesis."; Gene Expr. Patterns 3:219-223(2003).
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                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
Xenopodinae, Xenopus, Xenopus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred, No. 0.00039;
3; Mismatches 3; Indels
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EMBL; AF462392; AAQ04821.1; -.
SEQUENCE 1902 AA; 211461 MW; C61B9567A556E01E CRC64;
                                                                                                                               20-MAY-2004 (TrEMBLrel. 27, Created)
20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Rho-GTPase activating protein.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
KIAAL424 protein (Fragment).
Name-KIAA1424;
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                                                                                 PRT; 1902 AA
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PROSITE; PS50003; PH DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.7%;
Matches 16; Conservative
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SMART; SM00233; PH; 1.
SMART; SM00324; RhoGAP; 1.
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                                                                              PRELIMINARY;
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                                                                              AAQ04821
AAQ04821;
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29 P2(3)
AC 09 P2(3)
AC 09 P2(3)
AC 01 OO 01 OO 01 OO 01 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 OO 00 
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
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 Length 1944;
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                            4; Indels
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PROSITE; PS50003; PH DOMALN; 1.
PROSITE; PS50239; RHÖGAP; 1.
SEQUENCE 1957 AA; 217325 MW; 57C90CE6BB0FA164 CRC64;
                                                                                                                                                    QBNI19 PRELIMINARY; PRT; 1957 AA.
QBNI19;
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Rho-GTPage activating protein 10.
Name-ARGAP10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
Score 92; DB 2;
Pred. No. 0.0004;
5; Mismatches 4
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64.0%; Pred. No. 0.0004;
iive 5; Mismatches 4
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                                                                      1 MRDLPGHYYETLKFLVGHLKTIADH 25
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SEQUENCE FROM N.A.
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GAP_CAEEL
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SEQUENCE FROM N.A.

SEQUENCE 2238857; Pubmed=12477932;

Straums-2238857; Pubmed=12477932;

A Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh R.,

A Diatchento L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

B Diatchento L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abzamson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

B Fahey J., Helton E., Ketteman M., Maddan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                               Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S., Nakajima D., Nagase T., Ohara O., Koga H.;

"Prediction of the coding sequences of mouse homologues of XIAA gene:
II. The complete nucleotide sequences of 400 mouse KIAA-homologous
randomly sampled from size-fractionated libraries.";

DNA Res. 10:35-48(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%; Score 88; DB 2; Length 1262; 60.0%; Pred. No. 0.00099; ive 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             C9B320D3358C7D1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                         PERMY PRO0169; PH; 1.
PERMY PRO0169; PH; 1.
SMART; PRO0683; SPECTRINPH.
SMART; SM00233; PH; 1.
SMART; SE00334; RAGGAP; 1.
PROSITE; PS50031; PH DOMAIN; 1.
PROSITE; PS60142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1944 AA.
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574 IHDLPEHHFETLKFLSAHLKTVAEN 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRDLPGHYYETLKFLVGHLKTIADH 25
                                                                                                                                                                                                     MGD; MGI:1918685; Arhgap21.
InterPro; IPR006025; Pept_M Zn_BS.
InterPro; IPR011036; PH_related.
InterPro; IPR0011036; PH_related.
InterPro; IPR0011036; RhoGAP.
InterPro; IPR0010936; RhoGAP.
InterPro; IPR001605; Spectrin_PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                            TISSUE=Brain;
MEDLINE=22579291; PubMed=12693553;
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                                                                                                                                                                                         EMBL; AK122508; BAC65790.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0%
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                                                                SEQUENCE FROM N.A.
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                                      NCBI_TaxID=10090,
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SEQUENCE
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QEDEV3;
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Q6DFV3
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Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;
MEDLINE=94117490; PubMed=8288633;
Chen W., Blanc J., Lim L.;
"Characterization of a promiscuous GTPase-activating protein that has a bor-related domain from Caenorhabditis elegans.";
J. Biol. Chem. 269:820-823(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.5%; Score 88; DB 2; Length 1944; 60.0%; Pred, No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                            Strausberg R.,;
Submitted (UUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC076629; AAH76629.1; -.
SEQUENCE 1944 AA; 215741 MW; A7F832ECD3DBC081 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAP CAREL STANDARD; PRT; 1317 AA. P34289; Q85720; Q9TY64; P34289; P34589; Q85720; Q9TY64; O1-FEB-1994 (Rel. 28, Created) P.OCT--2003 (Rel. 42, Last sequence update) O5-UUL-2004 (Rel. 44, Last annotation update) GTPasse-activating protein GAP (CGGAP). Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.006; Mismatches
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1256 IHDLPEHHFETLKFLSAHLKTVAEN 1280
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STRAIN-C57BL/6; TISSUE-Head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.09
Matches 15; Conservative
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SEQUENCE FROM N.A.
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               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=22389257; PubMed=1247932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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Pred. No. 1.2;
                                                                                                                                                             EMBL; U02289; AAA18934.1; ALT_INIT.

EMBL; U16687; AAA71357.2; -..

EMBL; U16687; AAA71357.2; -..

EMBL; U16687; S44877.

R HSSP; Q07960; LRGP.

R HSSP; Q07960; LRGP.

R OO; G0.0005737; C:QVtoplasm; NAS.

GO; G0.0005109; F:RAS GTPase activator activity; IDA.

GO; G0.0005109; F:RAS GTPase activator activity; IDA.

GO; G0.0005109; F:RAS protein signal transduction; IDA.

R O; G0:0007265; P:RAS protein signal transduction; IDA.

GO; G0:0007265; P:RAS protein signal transduction; IDA.

R InterPro; IPR00189; PH.

InterPro; IPR00189; RhoGAP.

InterPro; IPR00189; RhoGAP.

InterPro; IPR00189; RhoGAP.

InterPro; IPR00189; RhoGAP.

R Pfam; PF00620; RhoGAP; 1.

R SMART; SM0023; PH; 1.

R SMART; SM0023; PH DOMAIN; 1.

R PROSITE; PS50238; RHOGAP; 1.
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660 858 Rho-GAP.
1064 1088 Ala-rich.
276 L -> I (in Ref. 1).
1317 Aa, 142069 MW; 5871763017001A39 CRC64;
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Last sequence update)
Last annotation update)
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5; Mismatches
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PH.
Gln-rich.
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nes 12; Conservative
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Mus musculus (Mouse)
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Maron D.M., Rodrigues S., Sanchez A., Mhiting M., Madan A., Rodrigues S., Sanchez A., Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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TISSUB=Skeletal muscle;

TISSUB=Skeletal muscle;

MEDLINE=97450957; PubMed=9305890;

Saras J., Franzen P., Aspenstrom P., Hellman U., Gonez L.J.,

Heldin C.H.;

A novel GTpsea-activating protein for Rho interacts with a PDZ domain of the protein-tyrosine phosphatase PTPLI.";

J. Biol. Chem. 272:24333-24338 (1997).

EMBL, 1090220; AABB1012.1;

PIR: E59430; E59430.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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R GO; GO:007242; P:intracellular signaling cascade; IEA.

R InterPro; IPR00219; DAG PE-bind.

R InterPro; IPR00198; RhoGAP.

R InterPro; IPR00198; RhoGAP.

R Pfam; PF00130; Cl; 1: 1.

R Pfam; PF00109; Cl; 1: 1.

R SWART; SW00109; Cl; 1.

R PROSITE; PS00479; DAG PE BIND DOM 1; UNKNOWN 1.

R PROSITE; PS0034; RHOGAP; 1.

R PROSITE; PS0031; RHOGAP; 1.

R PROSITE; PS0031; RHOGAP; 1.

R PROSITE; PS0031; RHOGAP; 1.

R PROSITE; PS0031; RHOGAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040387; AAH40387.1; -. HSSP; Q98935; 1F7C.
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GO, GO:0005100, F:Rho GTPase activator activity, TAS.
GO, GO:0007266, P:Rho protein signal transduction, TAS.
InterPro; IPR002219, DAG_PE-bind.
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01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-07N-1998 (TrEMBLrel. 26, Last annotation update)
PTPLI-ASSOCiated RhoGAP.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
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303 RKLPVHNYETLKFIMLHLNRVS 324
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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STRAIN-Bristol N2;
SIME M.A.;
SUBMITTED (NOV-1994) to the EMBL/GenBank/DDBJ databases.
SUBMI: 237093; CAA85469.2;
EMBL; 237093; CAA85469.2;
EMBL; 246812; CAA86848.2;
EMBL; 246812; CAA86848.2;
FIRE, T27959; T27959.

RINEL; 246812; FIREACELIULAR signaling cascade; IEA.
RINELFORD IRROGAP!
RINERFORD IRROGAP!
REAM, PF00620; RhoGAP; 1.
SWART; SM00109; RhoGAP; 1.
RNOSITE; PS50081; DAG PE_BIND_DOM_2; 1.
RNOSITE; PS50081; DAG PE_BIND_DOM_2; 1.
RYDOCHACICAL DACCEAIN.
RYDOCHACICAL DACCEAIN.
SEQUENCE 546 AA; 61969 MW; DAACC7221E729406 CRC64;
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44.8%; Score 64; DB 2; Length 546;
Best Local Similarity 54.5%; Pred. No. 1.3;
Matches 12; Conservative 4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                 50238; KHUGAP; 1.
1261 AA; 142105 MW; E4F7F56D7425DCE0 CRC64;
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Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTYSI8;
01-CCT-2003 (TrEMBLrel. 25, Created)
01-CCT-2003 (TrEMBLrel. 25, Last sequence update)
01-CCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein ZK669.1b.
InterPro; IPR000198; RhoGAP.

Pfam; PF00130; C1 1; 1.

Pfam; PF00130; C1 1; 1.

Pfam; PR00130; C1 1; 1.

SMART; SM00109; C1; 1.

PR0SITE; PS00479; DAG PE BIND DOM 1; UNKNOWN 1.

PROSITE; PS50081; DAG PE BIND DOM 2; 1.

PROSITE; PS50288; RHOGAP; 1.

SEQUENCE 1261 AA; 142105 MW; E4F7F56D7425DCE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    807 LRQLPASNENSLHFLIVHLKRVVDH 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRDLPGHYYETLKFLVGHLKTIADH 25
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 282:2012-2018(1998).
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EMBL; 237093 (CAA85468.2) ...
EMBL; 246812; CAA86847.2; JOINED.
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EMBL; 246812 (CAA86847.2) ...
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EMBL; 246812 (CAA86847.2) ...
EMBL; 246812 (CAA86847.2) ...
EMPC IPRO0139 (CAL5 FE Lind.
EMART; SM001039 (CAA867) ...
EMART; SM001039 (CAA87) ...
EMART; SM00103 (CAA867) ...
EMART; SM00103 (CAA97) ...
EMBL; PSS013; FCH; I...
EMPCSITE; PSS013; FCH; I...
EMPCSITE; PSS013; FCH; I...
EMPCSITE; PSS013; FCH; I...
EMPCSITE; PSS013; FCH; I...
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EMPCSTITE; PSS013; FCH; I...
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84.8%; Score 64; DB 2; Length 775;
Best Local Similarity 54.5%; Pred. No. 1.9;
Matches 12; Conservative 4; Mismatches 6; Indels
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STRALN-Baristol N2;
Thomas K.;
submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
Q27267, Q23573, Q23574, Q27267, Q27267, Q272573, Q23574, Q27267, Q27267, Q23573, Q23574, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q27267, Q2726
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:63950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
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Q6PCS4
ID Q6PCS.
AC Q6PCS.
DT 05-JUI
DT 05-JUI
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GN NAME =
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MEDINE=22388257; PubMed=12477932;

MEDINE=22388257; PubMed=12477932;

MEDINE=22388257; PubMed=12477932;

MEDINE=22388257; PubMed=12477932;

MALSTORE R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., A hischul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., A blatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E., Bromstein M.J., Usdin T.B., Toshiyuki S., Carninoi E., Mullahy S.J., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McEwran R.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Nilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Marra M.A., Shalska U., Smailus D.E., Schnerch A., Schein J.B., Schnerch A., Schein J.B., Schnerch A., Schein J.B., Schnerch A., Schein J.B., Scherzet D. M., Stalska U., Smailus D.E., Schnerch A., Schein J.B., Scherzet D. M. S., Stalska U., Smailus D.E., Schnerch A., Schein J.B., Stalska D. M., Stalska D., 
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955;
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Pred. No. 4.5;
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Strausberg R.;
Strausberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOS141, AAH59184.1; -
INTERPRO; IPR001395; Aldo/Ket red.
InterPro; IPR001219; DAG PE-bind.
InterPro; IPR001918; Rho_GAP.
Pfam; PF00130; Cl_1; 1.
Pfam; PF00130; Cl_1; 1.
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SWART; SM00109; CI; 1.

PROSITE; PS00063; ALDOKETO. REDUCTASE_3; UNKNOWN 1.

PROSITE; PS00061; DAG PE BIND DOM 1; UNKNOWN 1.

PROSITE; PS50081; DAG PE BIND DOM 2; 1.

PROSITE; PS50238; RHOĞAP; 1.

HYDOCHALICAL POCHAP: 147665 WW; 2061AE2507489079 CRC64;
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Best Local Similarity 41.7%;
Matches 10; Conservative
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Gaps

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6; Indels

8; Mismatches

Search completed: November 10, 2004, 13:38:30 Job time : 33.7478 secs

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Sequence 31, Appl
Sequence 29, Appl
Sequence 41, Appl
Sequence 61773, A
Sequence 61773, A
Sequence 48668, App
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 9, Appl
Sequence 9, Appli
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1 CGGRMEDIPCSRVGHIYRKY......YKVPAGVSLARNLKRVADWM
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-70-767-46209

US-09-270-767-46209

US-09-270-767-33441

US-09-270-767-3341

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         - protein search, using sw model
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APPLICANT: Donoho, Gregory
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Worke, James Alvin
APPLICANT: Wileke, James Alvin
APPLICANT: Potter, David George
TITLE OF INVENTION: POLYNICLEOTIDES ENCODING THE SAME
FILE REFERENT POLICATION NUMBER: US 60/185,920
PRIOR APPLICATION NUMBER: US 60/186,558
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENTH: 506
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US-09-710-279-2610
US-09-710-279-2610
US-09-307-621-2
US-09-710-279-2362
US-09-710-279-2362
US-09-718-070-4028
US-09-252-991A-18914
US-09-270-767-3646
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US-09-270-767-52063
US-09-83-110-4647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/09795926; Patent No. 6558669; GENERAL INFORMATION:
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 TYPE: PRT
, ORGANISM: homo sapiens
US-09-795-926-31
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APPLICANT: Kieke, James Alvin
APPLICANT: Kieke, James Alvin
APPLICANT: Kieke, James Alvin
APPLICANT: Kieke, James Alvin
APPLICANT: Potter, David George
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
FRIOR RELING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 60/185,920
PRIOR APPLICATION NUMBER: US 60/186,558
PRIOR APPLICATION NUMBER: US 60/191,849
PRIOR PLING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-03-04
SRIOR FILING DATE: 2000-03-04
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APPLICANT: Potter, David George
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
TITLE OF INVENTION: POLYNCLEOTIDES ENCODING THE SAME
FILE REPERRICE: LEX-0144-0228
CURRENT APPLICATION NUMBER: US 60/185,920
PRIOR APPLICATION NUMBER: US 60/185,920
PRIOR APPLICATION NUMBER: US 60/186,588
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/191,849
PRIOR PLILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/191,849
PRIOR SEQ ID NOS: 47
SOFTWARE: FRACESQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: DENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAEVWM 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAD-WM 42
                                                                                                               Abuin, Alejandro
Zambrowicz, Brian
Sands, Arthur T.
Walke, D. Wade
Wilganowski, Nathaniel L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilganowski, Nathaniel L.
            Donoho, Gregory
Hilbun, Erin
Turner, C. Alexander Jr.
Friedrich, Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 43, Application US/09795926 Patent No. 6555669 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zambrowicz, Brian
Sands, Arthur T.
Walke, D. Wade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: homo sapiens
US-09-795-926-29
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APPLICANT:
APPLICANT:
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Matches
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                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Sequence 6, Application US/09973457

Sequence 6, Application US/09973457

GENERAL INPORMATION:
TITLE OF INVENTION: 4174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
TITLE OF INVENTION: 4174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
TITLE OF INVENTION: 4009001

CURRENT PRILING APPLICATION NUMBER: US/09/973,457

CURRENT FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/238,849

PRIOR FILING DATE: 2000-10-06

NUMBER OF SEQ ID NOS: 6

SOFTWARRE: FastSEQ for Windows Version 4.0

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.8%; Score 217.5; DB 4; Length 631; Best Local Similarity 95.3%; Pred. No. 3.1e-24; Matches 41; Conservative 1; Mismatches 0; Indels 1.
Query Match 93.8%; Score 217.5; DB 4; Length 603; Best Local Similarity 95.3%; Pred. No. 2.9e-24; Matches 41; Conservative 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FILEGIEG, GLEIN, ALEMINA, APPLICANT: ADUIN, Alejandro
APPLICANT: Abunin, Alejandro
APPLICANT: Sands, Arthur T.
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Kieke, James Alvin
APPLICANT: Kieke, James Alvin
APPLICANT: Fotter, David George
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE
FILE REFERENCE: LEx-0144-USA
CURRENT APPLICATION NUMBER: US 60/195,920
PRIOR APPLICATION NUMBER: US 60/196,558
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-03-04
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PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE:
                                                                                                                                                                                                                                                            356 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAEVWM 398
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                                                                                                                                                                                                         1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
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Patent No. 6555669
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US-09-795-926-41
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Sequence 48658, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
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; ORGANISM: Drosophila melanogaster
US-09-270-767-33441
                                                                                                                                                                                                                                                                                                                Stewart, Timothy A
Tumas, Daniel
                                                                                                                                                                                  Gerritsen, Mary E.
Goddard, Audrey
                                              APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                             Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                            Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                   Filvaroff, Ellen
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                        Sherwood, Steven
Smith, Victoria
                                                                                                                  Desnoyers, Luc
Filvaroff, Ell
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 22; Conserva
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Best Local Similarity
Matches 23; Conserv
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US-09-270-767-33441
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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Sequence 61773, Application US/09270767

Sequence 61773, Application US/09270767

Sequence 61773, Application US/09270767

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

TILE REFERENCE: File Reference: 7326-034

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 61773

LENGTH: 290

LENGTH: 290
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326.094
CURRENT PAPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46209
                                                                                                                                                                                                       Gaps
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                                                                                                                                                      Query Match 51.9%; Score 120.5; DB 4; Length 149; Best Local Similarity 51.1%; Pred. No. 2.5e-10; Matches 24; Conservative 7; Mismatches 11; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.6%; Score 117.5; DB 4; Length 313; Best Local Similarity 53.3%; Pred. No. 1.7e-09; Matches 24; Conservative 4; Mismatches 14; Indels 3
                                                                                                                                                                                                                                                                      52 CGGRLEIVPCSHVGHVFRKRSPYIFPGKGSGKDVISRNIVRVAEVWM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 50.6%; Score 117.5; DB 4; Length I Similarity 53.3%; Pred. No. 1.6e-09; 24; Conservative 4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGRVEISPCSHVGHVFRSSTPYTFPGGMSEVLTDNLARAATVWM 56
                                                                                                                                                                                                                                               1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS----LARNLKRVAD-WM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS--LARNLKRVAD-WM 42
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                                                                                    ; OTHER INFORMATION: Consensus sequence US-09-973-457-6
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; Sequence 196, Application US/10140002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ; ORGANISM: Drosophila melanogaster US-09-270-767-46209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , TYPE: PRT
, ORGANISM: Drosophila melanogaster
US-09-270-767-61773
                         TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-270-767-46209
LENGTH: 149
                                                                 FEATURE
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOMOLIGE et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33441
LENGTH: 101
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33.04NLC59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 CGGSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWM 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGGRMEDIPCSRVGHIYRKYVPYKVPAG--VSLARNLKRVAD-WM 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 50.2%; Score 116.5; DB 4; Length 1 Similarity 51.1%; Pred. No. 4.7e-09; 23; Conservative 7; Mismatches 12; Indels
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5
APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48658
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: The Upjohn Company
APPLICANT: The Upjohn Company
APPLICANT: The Upjohn Company
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GaLNAc:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES:
ADDRESSEE: Pharmacia & Upjohn Company, Intellectual
ADDRESSEE: Property Legal Services
STREET: 301 Henrietta Street
CITY: Kalamazo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGGRMEDI PCSRVGHIYRKYVPYKVPAGVS -- LARNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 CGGILEIIPCSHVGHVFRDKSPYTFPGGVAKIVLHNAARVAEVWL 77
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llarity 44.4%; Pred. No. 5e-08;
Conservative 9; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,508
                                                                                                                                                                                                                                                                                                                                   Query Match
47.6%; Score 110.5; DB 4;
Best Local Similarity 48.9%; Pred. No. 5.1e-09;
Matches 22; Conservative 7; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 NO. 5910570ember 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4755.P CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-2210
TELEPAX: 616-833-8897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 19, Application US/08967508
; Patent No. 5910570
                                                                                                                                                                                                                                                                , ORGANISM: Drosophila melanogaster
US-09-270-767-48658
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TELEX: 224401
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 517 amino acids
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) MOLECULE TYPE: protein
US-08-967-508-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Michigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49001
                                                                                                                                                                                                                                           TYPE: PRT
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Sequence 19, Application US/08967506
Sequence 19, Application US/08967506
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Enceding a UDP-GaLNAC:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application PC/TUS9402552
Sequence 19, Application PC/TUS9402552
GENERAL INPORMATION:
APPLICANT: Blomery Ake P.
APPLICANT: Homa. Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GaLMAC:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Upjohn Company, Corp. Intellectual
ADDRESSEE: Property Law
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 CGGILEIVICSHVGHVFRKAIPYIFPGGIGGIINKNNRRLAEVWM 332
                           288 CGGTLBIVTCSHVGHVFRKATPYTFPGGTGQIINKNNRRLAEVWM 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS--LARNLKRVAD-WM 42
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1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS--LARNLKRVAD-WM
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pharmacia & Upjohn Company, Intellectual ADDRESSEE: Property Legal Services STREET: 301 Henrietta Street CITY: Kalamazoo STATE: Michigan COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/967,506 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.4%; Pred. No. 5e-08;
Matches 20; Conservative 9; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICATION:
PRICATION:
PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 No. 6096512ember 1995
ATTORNEY/AGENT INFORMATION:
NAME: DATAILY Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4755.P CP
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFRON: 616-833-2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        517 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 224401
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 517 amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-967-506-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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PCT-US94-02552-19
                                                                                                                       RESULT 12
US-08-967-506-19
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1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS--LARNLKRVAD-WM 42
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.2%; Score 109.5; DB 3;
44.4%; Pred. No. 5.4e-08;
Live 9; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PAIOR APPLICATION DATA:
APPLICATION UNDER: 08/602,830
FILING DATE: 13 No. 6095512ember 1995
ATORNEY/ACENT INFORMATION:
NAME: Darnley Jr., James D.
REGISCTRATION WUMBER: 33,673
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 616-833-2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 49001
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-967-506-9
; Sequence 9, Application US/08967506
; Patent No. 6096512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 301 Henrietta Street CITY: Kalamazco STATE: Michigan COUNTRY: USA
                                               TELBERAI: 616-833-boj.
TELEEX: 224401
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH = 559 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TYPE: Theat
                          TELECOMMUNICATION INFORMATION
    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 559 amino acids amino acids
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Best Local Similarity 44.43
Matches 20, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
Matches 20; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                        US-08-967-508-9
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Sequence 9, Application US/08967508

Sequence 9, Application US/08967508

Sequence 9, Application US/08967508

GENERAL INFORMATION:
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L. TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GALNAC:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Company, Intellectual ADDRESSE: Property Legal Services
STREET: 301 Henrietta Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
47.2%; Score 109.5; DB 5; Length 517;
Best Local Similarity 44.4%; Pred. No. 5e-08;
Matches 20; Conservative 9; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 CGGTLEIVTCSHVGHVFRKATPYTFPGGTGQIINKNNRRLAEVWM 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS--LARNLKRVAD-WM 42
                                                                                     ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02552
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 49001

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/08/967,508
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CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 No. 5910570ember 1995
FILING DATE: 13 No. 5910570ember 1995
ATCAREX FAGENT TROCRAMATION:
NAME: DATAILEY JI., James D.
REGISTRATION NUMBER: 33,673
                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4755.P CP
TELECOWNICATION INFORMATION:
TELEPHONE: 616-385-5210
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELERAX: 616-385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
301 Henrietta Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein PCT-US94-02552-19
                Kalamazoo
: Michigan
RY: USA
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: USA
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       CITY: Michay STATE: Michay COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: K
STATE:
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GENERAL INFORMATION:
APPLICANT: The Upjohn Company
APPLICANT: The Upjohn Company
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GalNAc:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Company, Intellectual
ADDRESSEE: Property Legal Services
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
47.2%; Score 109.5; DB 2; Length 559; 44.4%; Pred. No. 5.4e-08; Live 9; Mismatches 13; Indels 3;
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Search completed: November 10, 2004, 13:44:05 Job time : 15.5078 secs

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Sequence 32, Appl
Sequence 31, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 43, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
                                                                                                               November 10, 2004, 16:36:12 ; Search time 45.1192 Seconds (without alignments) 328.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                      232
1 CGGRMEDIPCSRVGHIYRKY.....YKVPAGVSLARNLKRVADWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-795-926-31

US-10-364-774-31

US-10-364-774-29

US-10-364-774-29

US-09-195-926-43

3 US-10-1851-2

US-10-364-774-43

US-10-364-774-43

US-10-364-774-41

US-10-364-368-35

US-09-374-358-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                 Copyright
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Match
                                                                                                                                                                                                                      Perfect score:
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                                                                                                                    Run on:
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14 137 59.1 62 15 US-10-410-764-35 Sequence 35, Appl 16 128.5 55.4 558 14 US-10-087-192-1989 Sequence 6, Appl 18 US-10-29-96-66 Sequence 1989, Appl 18 US-10-29-96-66 Sequence 6, Appl 18 US-10-187-192-1992 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-47 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1992, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 Sequence 1994, Appl 19 US-10-184-648-49 S
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## ALIGNMENTS

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US-10-092-750-32;
Sequence 32, Application US/10092750;
Publication No. US20030032157A1;
GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Maright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-XI
FILE REFERENCE: 5005/050002;
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT APPLICATION NUMBER: US 60/274.526
FRIOR APPLICATION NUMBER: US 60/274.526
MANBER OF SEQ ID NOS: 253
NUMBER OF SEQ ID NOS: 253
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-092-750-32

QUEST MATCH

GRANDIPCSRVCHIYRKIVPKYVPAGVSLARNLKRVADWM 42

ACGREDIPCSRVCHIYRKIVPYKVPAGVSLARNLKRVADWM 42

ACGREDIPCSRVCHIYRKIVPYKVPAGVSLARNLKRVADWM 42

RESULT 2
US-09-795-926-31
Sequence 31, Application US/09795926
FRENERAL INPORMATION:
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Gaps
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                                                                                                                               Query Match

93.8%; Score 217.5; DB 14; Length 506;
Best Local Similarity 95.3%; Pred. No. 8.2e-22;
Matches 41; Conservative 1; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Donono, Gregory
APPLICANT: Hilbur, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Milganowski, Nathaniel L.
APPLICANT: Wilganowski, Sames Alvin
APPLICANT: Wilganowski, NoveL HUWAN TRANSFERASE PROTEINS AND
ITILE OF INVENTION: NOVEL HUWAN TRANSFERASE PROTEINS AND
ITILE OF INVENTION: NOVEL HUWAN TRANSFERASE
TITLE OF INVENTION: NOVEL HUWAN TRANSFERASE
TITLE OF INVENTION: NOVEL USA
CURRENT PELLOR ON NOWBER: US 60/185,920
PRIOR APPLICATION NUMBER: US 60/186,558
PRIOR APPLICATION NUMBER: US 60/186,558
PRIOR APPLICATION NUMBER: US 60/191,849
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 29
ILENGTH: 535
ILENGTH: 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/10364774; Bublication No. US20030144497A1
GENERAL INPORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Abuln, Alejandro
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/09795926
Patent No. US20020098486A1
GENERAL INFORMATION:
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Ur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: homo sapiens
US-09-795-926-29
                    TYPE: PRT , ORGANISM: homo sapiens US-10-364-774-31
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US-09-795-926-29
     LENGIH: 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wiske, James Alvin
APPLICANT: Kieke, James Alvin
APPLICANT: Kieke, James Alvin
APPLICANT: Potter, David George
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE
TITLE OF INVENTION: NOVEL HUMAN
TITLE OF INVENTION: NOVEL HUMAN
TITLE OF INVENTION NUMBER: US/09/795,926
RRICR FILING DATE: 2001-02-29
RRICR FILING DATE: 2000-02-29
RRICR PILING DATE: 2000-02-29
RRICR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 31.
                                                                                                                                                                                                                                                 APPLICANT: Hu, YI.
APPLICANT: Hu, YI.
APPLICANT: Hu, YI.
APPLICANT: Kieke, James Alvin
APPLICANT: Kieke, James Alvin
APPLICANT: Kieke, James Alvin
APPLICANT: Potter, David George
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
FILE REFERENCE: LEX-0144-USA
CURRENT APPLICATION NUMBER: US 60/185,926
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
PRIOR PRIOR PRICATION NUMBER: US 60/186,556
PRIOR PLING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NOS: 47
LENGTH DO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAEVWM 301
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Donoho, Gregory
Hilbun, Erin
Turner, C. Alexander Jr.
Friedrich, Glenn
Abuin, Alejandro
Zambrowicz, Brian
Sands, Arthur T.
Walke, D. Wade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-364-774-31

s Sequence 31, Application US/10364774

; Publication No. US20030144497A1

; GENERAL INFORWATION:
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CRGANISM: homo sapiens
US-09-795-926-31
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1;

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18-10-101-851-2
Sequence 2, Application US/10001851
Sequence 2, Application US/10001851
Sequence 2, Application US/20020115628A1
SEQUENCE 3. Mo. US20020115628A1
GENERAL INFORMATION:
APPLICANT: WILLIAMSON, Mark
TITLE OF INVENTION: 47169 and 33935, No. US20020115628A1e1 Human Glycosyl Transferase
TITLE OF INVENTION: USes Thereof
FILE REPERENCE: 10147-56U1
CURRENT APPLICATION NUMBER: US/10/001,851
CURRENT PLING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/249,939
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ht.yaun.
APPLICANT: Hu, Yieke, James Alvin
APPLICANT: Hu, Yieke, James Alvin
APPLICANT: Kieke, James Alvin
APPLICANT: Kieke, James Alvin
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
TITLE OF INVENTION: DOLYNUCLEOTIDES ENCODING THE SAME
FILE REPERBRYCE: LEX-0144-USA
CURRENT APPLICATION NUMBER: US/10/364,774
CURRENT APPLICATION NUMBER: US/09/795,926
PRIOR APPLICATION NUMBER: US 60/186,528
PRIOR APPLICATION NUMBER: US 60/186,538
PRIOR PLILING DATE: 2000-02-29
PRIOR PLILING DATE: 2000-03-02
PRIOR PLILING DATE: 2000-03-02
PRIOR PLILING DATE: 2000-03-02
PRIOR PLILING DATE: 2000-03-04
PRIOR PLILING DATE: 2000-03-04
PRIOR PLILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NOS: 47
LENGTH: DD
                                                                                                                               356 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAEVWM 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAEVWM 398
                                                  1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAD-WM 42
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APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Walke, D. Wade
APPLICANT: Willey, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43, Application US/10364774
Publication No. US20030144497A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-851-2
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APPLICANT: Hu, Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Fotter, David George
J TILLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
TILLE OF INVENTION: NOVEL HUMAN THEANSFERASE PROTEINS AND
TILLE OF INVENTION: NOVEL HA-USA
CURRENT APPLICATION NUMBER: US/09/795,926
PRIOR APPLICATION NUMBER: US/09/795,926
PRIOR PLING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
PRIOR PLING DATE: 2000-02-29
PRIOR PLING DATE: 2000-02-29
PRIOR PLING DATE: 2000-02-30
PRIOR PLING DATE: 2000-02-40
PRIOR PLING DATE: 2000-03-02
PRIOR PLING DATE: 2000-03-04
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APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Potter, David George
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
TITLE OF INVENTION: DOLYNUCLEOTIDES ENCODING THE SAME
TITLE OF INVENTION: DOLYNUCLEOTIDES ENCODING THE SAME
FILE REPERENCE: LEx-0144-USA
CURRENT APPLICATION NUMBER: US 60/195,926
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 60/186,558
PRIOR PELING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
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PRIOR FILING DATE: 20
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Sands, Arthur T.
Walke, D. Wade
Wilganowski, Nathaniel L.
Hu, Yi
Kieke, James Alvin
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Turner, C. Alexander Jr.
Friedrich, Glenn
Abuin, Alejandro
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Patent No. US20020098486A1
GENERAL INFORMATION:
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Best Local Similarity 95.3
Matches 41; Conservative
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Score 217.5; DB 14; Length 631;
Pred. No. 1e-21;
1; Mismatches 0; Indels 1;
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
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86.4%; Score 200.5; DB 14;
Best Local Similarity 88.9%; Pred. No. 1.1e-19;
Matches 40; Conservative 1; Mismatches 1;
               HILE REFERENCE: LEX-O144-USA
CURRENT APPLICATION NUMBER: US/10/364,774
CURRENT FILING DATE: 2003-02-11
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US/09/795,926
PRIOR APPLICATION NUMBER: US 60/186,920
PRIOR APPLICATION NUMBER: US 60/186,58
PRIOR APPLICATION NUMBER: US 60/186,58
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-04
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FREESEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 41
LENGTH: 631
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Patent No. US20020107376A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.3%;
Matches 41; Conservative
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US-10-364-774-41
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US-10-292-896-3
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US-09-924-358-35
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                                           Query Match
93.8%; Score 217.5; DB 14; Length 603;
Best Local Similarity 95.3%; Pred. No. 1e-21;
Matches 41; Conservative 1; Mismatches 0; Indels 1;
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APPLICANT: Kiek, James Alvin
APPLICANT: Potter, David George
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
FILE REFERENCE: LEX-0144-013A
CURRENT APPLICATION NUMBER: US/09/795,926
CURRENT APPLICATION NUMBER: US 60/185,920
PRIOR PLING DATE: 2000-02-28
PRIOR PLING DATE: 2000-02-29
PRIOR PLING DATE: 2000-03-02
PRIOR PLING DATE: 2000-03-04
PRIOR PLING DATE: 2000-03-04
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 41
LUMING NA 11
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APPLICANT: Potter, David George
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Abuin, Alejandro
APPLICANT: Sambrowicz, Brian
APPLICANT: Gands, Arthur T.
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
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US-10-364-774-41
US-10-364-774-41
Sequence 41, Application US/10364774
Publication No. US20030144497A1
GENERAL INFORMATION:
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Turner, C. Alexander Jr.
Friedrich, Glenn
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Patent No. US20020098486A1
GENERAL INFORMATION:
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Sands, Arthur T.
Walke, D. Wade
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APPLICANT: Hilbun, Brin
APPLICANT: Turner, C. Alex
APPLICANT: Friedrich, Glen
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US-09-795-926-41
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US-1U-222-830-3
Sequence 3, Application US/10292896
Fublication No. US20030186850A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HASSAN, Hale
APPLICANT: BENNETT, ERIC P.
APPLICANT: CLAUSEN, Henrik
TITLE OF INVENTION: TRANSFERASES, PHRMACEUTICAL COMPOSITIONS COMPRISING SUCH AGENTS
TITLE OF INVENTION: TRANSFERASES, PHRMACEUTICAL COMPOSITIONS COMPRISING SUCH AGENTS
TITLE OF INVENTION: TRANSFERASES, PHRMACEUTICAL COMPOSITIONS COMPRISING SUCH AGENTS
TITLE OF INVENTION: TRANSFERASES, PHRMACEUTICAL COMPOSITIONS COMPRISING SUCH AGENTS
TITLE OF INVENTION: SUCH AGENTS FOR PREPARING MEDICAMENTS
TITLE OF INVENTION NUMBER: US 60/425,204
PRIOR PELICATION NUMBER: US 60/425,204
PRIOR PELICATION NUMBER: DC1010328
PRIOR PELICATION NUMBER: PC7/D01/0328
PRIOR FILING DATE: 2000-165-10
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
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13305, 14911, 86216,

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APPLICANT: Teai, Forgaring
APPLICANT: Teai, Forgaring
APPLICANT: Teai, Forgaring
APPLICANT: Call Cangaring
APPLICANT: Caroll, Osceph M.
TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
TITLE OF INVENTION WUMBER: US/10/410,764
CURRENT PILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/229,300
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-0-20
PRIOR PILING DATE: 2000-0-24
PRIOR APPLICATION NUMBER: US 60/351,572
PRIOR APPLICATION NUMBER: US 60/351,572
PRIOR APPLICATION NUMBER: US 60/236,654
PRIOR PILING DATE: 2000-10-2
PRIOR PILING DATE: 2000-10-2
PRIOR PILING DATE: 2000-10-2
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PRIOR PILING DATE: 2001-10-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452001122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR PRIOR PELING DATE: 2001-03-02
NUMBER OF EQ. ID NOS: 2059
SOFTWARE: FREUSED for Windows Version 4.0
SEQ ID NO 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.1%; Score 137; DB 15;
57.8%; Pred. No. 1.8e-11;
iive 8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Amino acid consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 seq 1D NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1989, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 57.8
Matches 26; Conservative
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APPLICANT: Machel Rangeth, Rachel TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226, AND TITLE OF INVENTION: 58764, TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS AND USES THEREFOR TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS AND USES THEREFOR CURRENT APPLICATION NUMBER: US/09/924,358
CURRENT APPLICATION NUMBER: US 60/229,300
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 137; DB 9; Length 62
Pred. No. 1.8e-11;
8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS---LARNLKRVAD-W 41
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Best Local Similarity 57.8%; Pred. No. 1.8e-11;
Matches 26; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/10133709
| Publication No. US20030181343A1
| GENERAL INFORMATION:
| APPLICANT: Meyers, Rachel
| APPLICANT: Meyers, Rachel
| TITLE OF INVENTION: 47153, A HUMAN GLYCOSYLTRANSFERASE
| TITLE OF INVENTION: PAMILY MEMBER AND USES THEREFOR
| FILE REFERENCE: 38152005200
| CURRENT APPLICATION NUMBER: US/10/133,709
| CURRENT APPLICATION NUMBER: 60/279,647
| PRIOR APPLICATION NUMBER: 60/279,647
| RICHARD FILING DATE: 2001-03-28
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 9
| LENGTH: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Consensus amino acid sequence US-10-133-709-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-4...

Sequence 15, Appliant...

Sequence 15, Appliant...

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc...

APPLICANT: Meyers, Rachel E...

APPLICANT: MacBeth, Kyle J...

APPLICANT: Curtis, Rory A.J...

APPLICANT: Rudolph-Owen, Laura A.

TANT: Weich, Nadine S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Consensus amino acid
US-09-924-358-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.8%;
Matches 26; Conservative
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ORGANISM: Artificial Sequence
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US-10-410-764-35
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Gaps

us-10-092-750-32.rapb

Query Match 55.4%; Score 128.5; DB 13; Length 539; Best Local Similarity 55.6%; Pred. No. 3e-09; Matches 25; Conservative 6; Mismatches 11; Indels 3; Gaps

7

1 CGGRMEDIPCSRVGHIYRKYVPYKVP--AGVSLARNLKRVAD-WM 42 ||| :| ||||||||::|| || || :| || || :| || 326 CGGSLEIIPCSRVGHVFRKQHPYTFPGGSGTVFARNTRRAAEVWM 370

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Search completed: November 11, 2004, 01:28:14 Job time : 46.1692 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein November 10, Run on:

2004, 12:29:32; Search time 9.35751 Seconds (without alignments) 431.857 Million cell updates/sec

US-10-092-750-32 232 1 CGGRMEDIPCSRVGHIYRKY.....YKVPAGVSLARNLKRVADWM 42 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |                |          |       |          |       |       |                    |       |                    |                    |                    |       |                    |                    |       |                    |                    |      |      |      |                    |    | -    |                    |                    |                    |                    |                    |              |                    |
|-----------|----------------|----------|-------|----------|-------|-------|--------------------|-------|--------------------|--------------------|--------------------|-------|--------------------|--------------------|-------|--------------------|--------------------|------|------|------|--------------------|----|------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------|--------------------|
|           | Description    | cal prot | ż     | cal prot | N-ace | N-ace | polypeptide N-acet | ypept | probable polypepti | polypeptide N-acet | polypeptide N-acet | N-ace | probable polypepti | polypeptide N-acet | N-ace | polypeptide N-acet | polypeptide N-acet | 14   | ż    | z    | hypothetical prote | IJ | prot | p53-binding protei | vesicular transpor | H+-transporting tw | UDPglucose 4-epime | dihydroorotate deh | c shock prot | molecular chaperon |
|           |                |          |       |          |       |       |                    |       |                    |                    |                    |       |                    |                    |       |                    |                    |      |      |      |                    |    |      |                    |                    |                    |                    |                    |              |                    |
| S         |                |          |       |          |       |       |                    |       |                    |                    |                    |       |                    |                    |       |                    |                    |      |      |      |                    |    |      |                    |                    |                    |                    |                    |              |                    |
| SUMMARIES |                | 52       | 05    | 30       | 20    | 49    | 48                 | 44    | 45                 | 47                 | 46                 | 15    | 43                 | 23                 | ~     |                    |                    | •    | 10   | •#   | •                  | 46 | 02   | 04                 |                    |                    | 26                 |                    |              |                    |
| ស         |                | ı ın     | 4     | T269     | T4225 | T422  | Ň                  | N.    | $\sim$             | $\sim$             | N                  | ı۸    | $\sim$             | $\sim$             | A459  | JC524              | T422               | T273 | T422 | T315 | A378               | 9  |      | 36                 | 겁                  | 9                  | m                  | 719                | 417          | 970                |
|           | DB             | 2        | 0     | 7        | 7     | ~     | 7                  | 0     | ~                  | ~                  | 0                  | N     | 7                  | N                  | N     | 0                  | ~                  | ~    | 7    | ~    | 0                  | ~  | N    | ~                  | ~                  | н                  | ~                  | N                  | N            | N                  |
|           | Length         | 7        | 7     | 684      | 9     | Н     | Н                  | œ     | $^{\circ}$         | $^{\circ}$         | S                  | ø     | Ħ                  | S                  | S     | 3                  | 0                  | 0    | 3    | 2    | 2                  | ın | 54   | S                  | σ                  | m                  | 0                  | S                  | ~            | _                  |
| de        | Query<br>Match | . 6      | ď.    | 51.9     | ö     | ö     | ö                  | ď.    | φ.                 | ٥.                 | σ,                 | o,    | φ.                 | ۲.                 | ۲.    | ŝ                  | ö                  | ö    | ö    | σ,   | 4                  | 4. | 4.   | 4.                 | 4.                 | 4.                 | m.                 | m,                 | m.           | 23.7               |
|           | Score          | 00       | 128.5 | 20       | н     | н     | 11                 | 115.5 | -                  | -                  | 11                 | 14.   | 14,                |                    | 99.   | 0                  | 94                 | 94   | Φ    | 90.5 | 7                  | 57 | 57   | 57                 | 56.5               | 56                 | 22                 | 52                 | 52           | 55                 |
|           | Result<br>No.  |          | 7     | m        | 4     | ហ     | 9                  | 7     | 80                 | 6                  | 10                 | 11    | 12                 | 13                 | 14    | 15                 | 16                 | 17   | 18   | 19   | 20                 | 21 | 22   | 23                 | 24                 | 25                 | 56                 | 27                 | 28           | 53                 |

| cysteine proteinas hypothetical prote argininosuccinate hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable AMP-bindi hypothetical prote arsenate reductase uracil phosphoribo hypothetical prote hypothetical prote arsenate reductase uracil phosphoribo hypothetical prote hypothetical prote cytochrome P450 ka 1,4-alpha-glucan b                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | RESULT 1  TALIGNMENTS  RESULT 1  TALIGNMENTS  Hypotherical protein DKFZp586H0623.1 - human (fragments)  C,Species: Homo sapiens (man)  C,Species: Homo sapiens (man)  C,Accession: T1252  R,Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  R,Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  R,Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Accession: T1252  A,Acces |
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| попропопопопоп                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 106;<br>2 red 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
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polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - human polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - human C;Species: Homo sapiens (man)
C;Species: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004
C;Accession; 137405
C;Accession; 137405
A;Ritle: Purification and cDNA cloning of a human UDP-GalNAC;polypeptide N-Acetylgalactos A;Reference number: 137404; MUD: 56025800; PMID: 592619
A;Reference number: 137405

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-571 <RES>

A, Cross-references: UNIPROT:Q10471; EMBL:X85019; NID:g971460; PIDN:CAA59381.1; PID:g97146 Genetics:
A, Genetics:
A, Grantics:
A, Cross-references: GDB:696223
A, Tross-references: GDB:69624
C, Superfamily: polypebtide Nacetylgalactosaminyltransferase
C, Superfamily: polypebtide Nacetylgalactosaminyltransferase
C, Keywords: glycosyltransferase; hexosyltransferase

Length 571; 55.4%; Score 128.5; DB 2; Query Match

25:

Best Loca Matches

C, Accession: T26930 R, McMurray, A.

RESULT 3

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R,Hagen, F.K.; Nehrke, K.
J. Biol. Chem. 273, 8268-8277, 1998
J. Biol. Chem. 273, 8268-8277, 1998
A,Title: cDNA cloning and expression of a family of UDP-N-acetyl-Dgalactosamine:Polypepti A,Reference number: Z22126; MUID:98192620; PMID:9525933
A,Accession: 142249
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-617 < RAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec.1999 #text_change 09-Jul-2004 C;Date: 03-Dec.1999 #text_change 09-Jul-2004 C;Dates: 03-Dec.1999 #text_change 09-Jul-2004 C;Dates: 03-Merke, K. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J. Nehrke, K. J.
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R:Haggn, F.K.; Nebrke, K.
J. Balol. Chem. 273, 8268-8277, 1998
A;Title: cDNA cloning and expression of a family of UDP-N-acetyl-Dgalactosamine:Polypepti
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A;Introns: 42/3; 64/3; 154/1; 202/1; 368/3; 430/1; 477/3; 513/3; 563/3; 604/3
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C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGGRMEDIPCSRVGHIYRKYVPYKVP---AGVSLARNLKRVAD-WM 42
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C;Superfamily: polypeptide N-acetylgalactosaminyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: gly-6
C;Superfamily: polypeptide N-acetylgalactosaminyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase
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A;Residues: 1-618 <HAG>
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Matches
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R;Hagen, F.K.; Nehrke, K.
Biol. Chem. 273, 8268-8277, 1998
A;Title: CDNA cloning and expression of a family of UDP-N-acetyl-Dgalactosamine:Polypept A;Reference number: Z22126; MUID:98192620; PMID:9525933
A;Accession: T42250
A;Accession: T42250
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Reture type: mRNA
A;Reture type: mRNA
A;Residues: 1-562 <HAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:045947; EMBL:AL021492; PIDN:CAA16378.1; GSPDB:GN00022; CESP:
A;Experimental source: clone Y45F10D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) 6c - Caenorhabditis elegans C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42249
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ب
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                        1 CGGRMEDIPCSRVGHIYRKYVPYKVP--AGVSLARNLKRVAD-WM 42
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C;Superfamily: polypeptide N-acetylgalactosaminyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:Y45P10D.3
A;Map position: 4
A;Introns: 61/3; 112/1; 142/3; 178/3; 230/3; 289/2; 611/2
C;Superfamily: polypeptide N-acetylgalactosaminyltransferase
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                                             Pred. No. 3.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-684 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, January 1998
A;Reference number: 220288
A;Accession: T26930
                                                                                       6; Mismatches
                                             ilarity 55.6%;
Conservative
                                                  Local Similarity
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Genetics:

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polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: Ca-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C,Accession: T42246 R,Hagen, F.K., Nehrke, K. J. Biol. Chem. 273, 8268-8277, 1998 A,Title: CDNA cloning and expression of a family of UDP-N-acetyl-Dgalactosamine:Polypept: A,Reference number: Z22126; MUD:98192620; PND:9525933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide N-acetylgalactosaminyltransferase homolog - Caenorhabditis elegans
Cippecias Caenorhabditis elegans
Ciptecias: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Nov-2001
C;Accession: A88515
C;Accession: A88515
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A;Rofor) MID:99066613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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Cyspecies Caenorhabditis elegans
Cyspecies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
CyAccession: T42243, 844913
R;Hagen, F.K.; Nehrke, K.
B;Hagen, F.K.; Nehrke, K.
J. Báol. Chem. 273, 8268-8277, 1998
A;Title: cDNA cloning and expression of a family of UDP-N-acetyl-Dgalactosamine:Polypepti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:061392; EMBL:AF031836; NID:93047192; PIDN:AAC13672.1; PID:93
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A;Residues: 1-563 <STO>
A;Cross-references: GB:chr_III; PIDN:AAA28224.1; PID:g289776; GSPDB:GN00021
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                                             390 CGGTLEIVPCSHVGHVFRKRSPYKWRTGVNVLKRNSIRLAEVWL 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 CGGTLEIVPCSHVGHVFRKRSPYKWRTGVNVLKRNSIRLAEVWL 433
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Local Similarity 52.3%; Pred. No. 2.4e-07;
Nes 23; Conservative 8; Mismatches 11; Indels
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C,Superfamily: polypeptide N-acetylgalactosaminyltransferase
C,Keywords: glycosyltransferase; hexosyltransferase
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C,Superfamily: polypeptide N-acetylgalactosaminyltransferase
            1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS-LARNLKRVAD-WM
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-626 <HAG>
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Best Local Similarity
Matches 22; Conserv
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R;Hagen, F.X.; Nebrke, K.
R;Hagen, F.X.; Nebrke, K.
J. Blol. Chem. 273, 8268-8277, 1998
A;Title: CDNA cloning and expression of a family of UDP-N-acetyl-Dgalactosamine:Polypept
A;Keférence number: 222126; MUID:98192620; PMID:9525933
A;Accession: T42245
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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C;Species: Caenorhabditis elegans
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A;Cross-references: UNIPROT:O61391; EMBL:AF031835; NID:g3047190; PIDN:AAC13671.1; PID:g3
                                                                                                                  Residues: 1-589 <HAG>
;Cross-references: UNIPROT:061390; EMBL:AF031834; NID:g3047188; PIDN:AAC13670.1; PID:g3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Caenorhabditis elegans
| Species: Caenorhabditis elegans
| Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 115; DB 2; Length 623;
Pred. No. 2.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 CGGSLEIMPCSRVGHVFRKKHPYTFPGGSGNVFQKNTRRAAEVWM 404
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS--LARNLKRVAD-WM 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS-LARNLKRVAD-WM 42
A;Reference number: 222126; MUID:98192620; PMID:9525933
A;Accession: T42244
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-589 <HAG>
A;Cross-references: UNIPROT:061390; EMBL:AF031834; NID:g30471
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: polypeptide N-acetylgalactosaminyltransferase
C;Reywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: gly-5
C,Superfamily: polypeptide N-acetylgalactosaminyltransferase
C,Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                   49.8%; Score 115.5; DB 2
48.9%; Pred. No. 1.9e-07;
tive 7; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                                                            22; Conservative
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Best Local Similarity
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A;Reference number: Z22126; MUID:99192620; PMID:9525933 A;Accession: T42243 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA

A; Residues: 1-612 < HAG>

```
F.-free: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
CjoBecie: Bas primigentus taurus (Cattle)
CjoAccession: A45987; A8530
B;Homa, F.L.; Hollander, T.; Lehman, D.J.; Thomsen, D.R.; Elhammer, A.P.
J. Biol. Chem. 268, 12609-12616, 1993
A;Title: Isolation and expression of a cDNA clone encoding a bovine UDP-GalNAc:polypeptic, A;Reference number: A45987; MUID:93286099; PMID:7685345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q07537; GB:L07780; NID:g289411; PIDN:AAA30532.1; PID:g289412 A;Cross-references: UNIPROT:Q07537; GB:L07780; NID:g289411; PIDN:AAA30532.1; PID:g289412 A;Note: authors translated the codon GAT for residue 310 as Agn
R;Hagen, F.K.; VanWuyckhuyse, B.; Tabak, L.A.
J. Biol. Chem. 268, 18960-18965, 1993
A;Title: Purification, cloning, and expression of a bovine UDP-GalNAc: polypeptide N-acet A;Reference number: A48530; MUID:93366815; PMID:8360184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Wolecule type: mRNA
A; Residues: 1-633 < CARA.
A; Residues: 1-633 < CARA.
A; Cross-references: UNIPROT: P70419; GB:U70538; NID:g1575722; PIDN:AAB09579.1; PID:g15757;
A; Experimental source: testis extraction of N-acetyl-D-galactosamine alpha-O-Ser/Th
C; Comment: This enzyme extalyzes the formation of N-acetyl-D-galactosamine alpha-O-Ser/Th
itiating O-glycosylation of serine and threonine resides on an array of glycoproteins.
C; Superfamily: polypeptide N-acetylgalactosaminyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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C;Superfamily: polypeptide N-acetylgalactosaminyltransferase
C;Reywords: colostrum; glycosyltransferase; hexosyltransferase
                                                                                                                                                                              polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 CGGTLEIVTCSHVGHVFRKATPYTFPGGTGQIINKTNRLAEVWM 374
330 CGGTLEIVTCSHVGHVFRKATPYTFPGGTGQIINKNNRRLAEVWM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS--LARNLKRVAD-WM 42
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Pred. No. 1.2e-06;
9; Mismatches 13; Indels
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46.6%; Score 108; DB 2; Length 63
Best Local Similarity 47.7%; Pred. No. 2.1e-06;
Matches 21; Conservative 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS-LARNLKRVAD-WM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: November 10, 2004, 13:40:40 Job time : 10.3575 secs
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Best Local Similarity 44.4%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 41-559 <HAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-559 <HOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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                                                                                                                                                                              A.Cross-references: UNIPROT:P34678, EMBL:AF031833, NID:g3047186, PIDN:AAC13669.1, PID:g3 R;Wilson, R. Ebbild to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid ZK688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA

A; Residues: 1-559 <MED.

A; Cross-references: UNIPROT:Q10472

A; Cross-references: UNIPROT:Q10472

A; Cross-references: UNIPROT:Q10472

A; Note: The authors translated the codon AAT for residue 264 as Asp

A; Note: The authors translated the codon AAT for residue 264 as Asp

A; Note: The authors translated the codon AAT for residue 264 as Asp

A; Note: The authors translated the codon AAT for residue 264 as Asp

A; Note: The authors translated from GB/EMBL/DDBJ

A; Reference number: 137404

A; Reference number: 137404

A; Releases preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X85018; NID:g971458; PIDN:CAA59380.1; PID:g971459
C;Comment: This enzyme catalyzes the initial reaction in O-linked (mucin type) oligosacd exterpy pathway.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Map position: 18
C; Superfamily: polypeptide N-acetylgalactosaminyltransferase
C; Superfamily: polypeptide N-acetylgalactosaminyltransferase; hexosyltransferase; C; Superfamily: polypeptide N-acetylgalactosin; glycosyltransferase; hexosyltransferase; C; Sey Momain: transmembrane #status predicted c TMM
F; 29-559/Domain: endoplasmic reticulum lumenal #status predicted c TMM
F; 59: 141, 541, 552, Brinding site: carbohydrate (Asn) (covalent) #status predicted
F; 117, 118, 288/Binding site: carbohydrate (TMT) (covalent) #status predicted
F; 119/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - human Nylternate names: GalNAc-transferase (EC 2.4.1.41) - human Nylternate names: GalNAc-transferase (EC 2.4.1.41) - human Saplanes (man) (Spacesies: Home saplanes (man) (Spacesies: Hawv-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004 (Spacession: JG4223; I37404 (Spacession: JG4223; I37404 (Spacession: JR, Naylor, J.M.; Baker, C.A.; Thomsen, D.R.; Homa, F.L.; Elhammer, A.P. J. Biochem. 118, 568-574, 1995 (Spacession, and chromosomal localization of a human UDP-GalNAc: A; Reference number: JG4223; MUID:96115928; PMID:8690719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                         A,Accession: $44913
A,Molecule type: DNA
A,Residues: 50-612 <MIL>
A,Cross-references: EMBL:L16621; NID:g289775; PIDN:AAA28224.1; PID:g289776
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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m ..

Score 114.5; DB 2; Length Pred. No. 2.8e-07; 6; Mismatches 14; Indels

Query Match
Best Local Similarity 48.9%;
Matches 22; Conservative

A; Introns: 101/1; 229/3; 520/3; 570/3 C; Superfamily: polypeptide N-acetylgalactosaminyltransferase C; Keywords: glycosyltransferase; hexosyltransferase

Gene: gly-3

384 CGGSLEIHPCSRVGHVFRKQTPYTFPGGTAKVIHHNAARTAEVWM 428

1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS--LARNLKRVAD-WM 42

Score 109.5; DB 2; Length Pred. No. 1.2e-06; 9; Mismatches 13; Indels

Query Match Best Local Similarity 44.4%; Matches 20; Conservative

A; Residues: 1-559 < RES>

Accession: JC4223

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 10, 2004, 12:27:34 ; Search time 51.285 Seconds (without alignments) 471.205 Million cell updates/sec

Run on:

US-10-092-750-32 232 1 CGGRMEDIFCSRVGHIYRKY.....YKVPAGVSLARNLKRVADWM 42 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0°, Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

|               |       | æ              |        |     | SUMMARIES         |                    |
|---------------|-------|----------------|--------|-----|-------------------|--------------------|
| Result<br>No. | Score | Query<br>Match | Length | DB  | П                 | Description        |
| -             | 217.5 |                | 603    | ! ~ | GL10 HIMAN        | O86srl h polypepti |
| N             | 217.5 | ٠<br>س         | 603    | -   | GL10_MOUSE        | 060987 m polypepti |
| m             | 217.5 | 93.8           | 603    | Н   | GL10 RAT          | 0925r7 r polypepti |
| 4             | 217.5 |                | 603    | N   | AAH60617          | Aah60617 mus muscu |
| ß             | 217.5 | ω.             | 634    | Ŋ   | BAD21405          | Bad21405 mus muscu |
| 9             | 143   | ij             | 599    | N   | Q7PZMS            | Q7pzm5 anopheles g |
| 7             | 131   | 56.5           | 644    | N   | Q7Q0E9            | 07q0e9 anopheles q |
| 80            | 128.5 |                | 558    | Н   | GTL1 HUMAN        | 08n428 h putative  |
| σ             | 128.5 | 55.4           | 558    | Н   | GTL1 MOUSE        |                    |
| 10            | 128.5 | 55.4           | 570    | Н   | GLT2_MOUSE        | Q6pb93 m polypepti |
| 11            | 128.5 | 55.4           | 570    | (1) | AAH59818          | Aah59818 mus muscu |
| 12            | 128.5 | ď.             | 571    | Н   | GLT2 HUMAN        | Q10471 h polypepti |
| 13            | 128   | 55.2           | 1003   | 7   | Q7QDR0            | Q7qdr0 anopheles g |
| 14            | 126.5 | 4.             | 290    | N   | AAS64620          | Aas64620 drosophil |
| 15            | 126.5 | 4.             | 615    | N   | AAQ56700          |                    |
| 16            | 126.5 | 4.             | 633    | Н   | GLT2_DROME        |                    |
| 17            | 126   | 4.             | 351    | N   | 0700X9            | Q7q0x9 anopheles g |
| 18            | S     | 'n             | 620    | N   | 070456            | Q7q456 anopheles g |
| 19            | 120.5 | ä              | 622    | Н   | GL10 CAREL        | enorhabd           |
| 20            | 118   | 50.9           | 518    | N   | 070048            | ophele             |
| 21            | 118   | ö              | 650    | Н   | GLT9 DROME        | Osmrc9 drosophila  |
| 22            | 117.5 | 。              | 667    | Н   | GLT3_DROME        | Q9y117 drosophila  |
| 53            | 116.5 | ö              | 550    | Н   | GL14 MOUSE        | Q8bvg5 m polypepti |
| 24            | 116.5 | ö              | 552    | Н   | GL14 HUMAN        | Q96fl9 h polypepti |
| 25            | 116.5 | ö              | 552    | N   | AAQ8 <u>9</u> 118 | Aag89118 homo sapi |
| 56            | 116.5 | 。              | 645    | 7   | Q7Q815            | Q7q8i5 anopheles g |
| 27            | 116   | 。              | 618    | Н   | GLT6 CAREL        | O61394 caenorhabdi |
| 28            | 115.5 | 6              | 589    | Н   |                   | Q8i136 caenorhabdi |
| 59            | 115   |                | 626    | Н   | GLTS CAEEL        | Q95zjl caenorhabdi |
| 30            | 114.5 | 49.4           | 612    | М   | GLT3_CAEEL        |                    |
| 31            | 114   | 49.1           | 622    | н   | GLT6_HUMAN        | Q8nc14 h polypepti |
|               |       |                |        |     |                   |                    |

| Q8c7u7 m polypepti<br>Q8422 r polypepti<br>Q72m9 h polypepti<br>Q6is24 h putative<br>Q7tt15 m putative<br>AAh67524 homo sapi<br>AAh67525 homo sapi<br>AAh69624 homo sapi<br>AAh69636 homo sapi<br>AAh69636 homo sapi<br>AAh69636 homo sapi<br>AAh69937 homo sapi<br>AAh69937 homo sapi<br>AAh69937 homo sapi<br>Q8c102 m polypepti<br>Q8c102 m polypeptia |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| GLTE_MOUSE<br>GLTS_RAT<br>GLTS_HUMAN<br>GTL3_HUMAN<br>GTL3_MOUSE<br>AAH67525<br>AAH69628<br>AAH69636<br>AAH69636<br>AAH69636<br>AAH69636<br>AAH69636<br>AAH69636                                                                                                                                                                                          |
|                                                                                                                                                                                                                                                                                                                                                           |
| 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                   |
| 4444444444444<br>000000000000000000000000                                                                                                                                                                                                                                                                                                                 |
| 11.13.14<br>11.13.15<br>11.12.15<br>11.12.15<br>11.12.15<br>11.12.15<br>11.12.15<br>11.12.15<br>11.13.15                                                                                                                                                                                                                                                  |
| -                                                                                                                                                                                                                                                                                                                                                         |

# ALIGNMENTS

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REP N. (ISOFORM 2)

REPORTED AND CONTROL 2.

REA TISSUE-Placenta, and Spleen,

REA CLAIN STATE TO COURT T., Sugiyama T., Irie R.,

REA CLAIN STATE T., CALONIA T., Shibahara T., Tanaka T., Ishia S.,

REA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishia S.,

REA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishia S.,

REA Sekine M., Takhashi M., Tsono Y., Nakamura Y.,

RA Manatori A., Rudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RA Shiratori A., Sudo H., Kimata M., Watanabe M., Hiracka S., Chiba Y.,

RA Samazaki M., Ninomiya K., Takhashi T., Yamashita H., Murakawa K.,

RUJimori K., Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T.,

RUSANO J., Ranehori K., Takhashi Pujii A., Hara H., Ranasa T.-O.,

RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,

RUSANO J., Ranehori K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

ROSHIKAWA Y., Mateunawa H., Satch N., Takami S., Torashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Pujimori Y., Komiyama H., Satch N., Takami S., Pikuzumi Y.,

RA Nakagawa S., Senoh A., Mizoguchi A., Takura S., Pikuzumi Y.,

RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Pikuzumi Y.,

RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Pikuzumi Y.,

RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Pikuzumi Y.,

RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Pikuzumi Y.,

RA Hishigaki H., Watanabe Y., Sonjumi Y., Senba T.,

RA Vijimori Y., Manajima Y., Moguno Y., Shimizu T.,

RA Wabata A., Hikiji T., Kobatake N., Inagaki H., Ikwabata A., Hikiji T., Kobatake N., Inagaki H., Ikwabata A., Hikiji T., Kobatake N., Kumada Y., Okamoto S.,

RA Matsumura K., Nakajima Y., Mizuno T., Shirai R., Yamaahita R.,

RA Makai K., Yada T., Nomura Y., Ohara O., Isogai T., Sugano S.,

RA Wakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

R
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schnein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 8-366 FROM N.A. (ISOFORM 3), AND SEQUENCE OF 117-603 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isoid=Q86SR1-5; Sequence=VSP_011210, VSP_011211;
Note=No experimental confirmation available;
-!- TISSUE SPECIFICITY: Widelly expressed. Expressed at high level in small intestine, and at intermediate levels in stomach, pancreas, ovary, thyroid gland and spleen. Weakly expressed in other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isold=Q86SR1-4; Sequence=VSP_011207, VSP_011208, VSP_011214;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Genet. 36:40-45(2004).

-!- FUNCTION: Catalyzes the initial reaction in O-linked

-!- oligosaccharide biosynthesis, the transfer of an N-acetyl-D-galactosamine residue to a serine or threonine residue on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein receptor. Has activity toward Muc5Ac and EA2 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UDP + N-acetyl-D-galactosaminyl-polypeptide.
--- COFACTOR: Mangae and calcium (By similarity).
--- PATHMAY: Glycosylation.
--- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q86SR1-3; Sequence=VSP_011212, VSP_011213;
Note=No experimental confirmation available;
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Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=086SR1-1; Sequence=Displayed;
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ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substrates.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
               -!- DOMAIN: There are two conserved domains in the glycosyltransferase region: the N-terminal domain (domain A, also called GT1 motif), which is probably involved in manganese coordination and substrate binding and the C-terminal domain (domain B, also called Gal/GalNac-T motif), which is probably involved in catalytic reaction and UDP-Gal binding (By similarity).
-!- DOMAIN: The ricin B-type lectin domain binds to GalNac and contributes to the glycospeptide specificity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform 4).
/FIId=VSP 011207.
WELGCYDPGIEIWGGEQYEISFK -> MLAWRDGELEAETS
                                                                                                                                                                                                                                                             -!- SIMILARITY: Contains 1 ricin B-type lectin domain.
-!- CAUTION: According to experiments made in rat, this enzyme is unable to transfer GalNAc onto serine or threonine recidue on the protein receptor, but instead requires the prior addition of a GalNAc on a peptide before adding additional GalNAc moieties, thereby acting as a glycopeptide transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catalytic subdomain A.
Catalytic subdomain A.
Catalytic subdomain B.
Ricin B-type lectin.
By similarity.
By similarity.
By similarity.
N.linked (GlCNAc. ..) (Potential).
N.linked (GlCNAc. ..) (Potential).
N.linked (GlCNAc. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLM; VOUSUS; MINIOLITIS; GIYCO trans 2.
INTERPRO; IPRO08997; Ricins like.
INTERPRO; IPRO08997; Ricins lectin.
Pfam; PF00552; Glycos transf 2; 1.
Pfam; PF00552; Ricins lectin; 3.
SWART; SW00458; RICIN; 1.
SWART; SW00458; RICIN; 1.
Alternative splicing; Calcium; Glycosyltransferase; Golgi stack; Lectin; Manganese; Signal-anchor; Transferase; Transmembrane.
DOMAIN.

11. Cytoplasmic Rocential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal-anchor for type II membrane
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/FTId=VSP_011208.
Missing (In isoform 2).
/FTId=VSP_011209.
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/FTId=VSP_01121u.
Missing (In isoform 5).
/mra-usp_011211.
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Lumenal (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB078145; BA556890.1; EMBL; AL096739. CAD44532.1; EMBL; AL096739. CAD44532.1; EMBL; BC0072245; AA407224.2; EMBL; BC0072245; AA450333.1; EMBL; BC072456, AA472450.1; EMBL; AX074132; BAB14676.1; ATT_INIT.EMBL; AX074132; BAB84958.1; EMBL; AX074132; BAB84958.1; EMBL; AX074132; EMBL; EMBL; AX074132; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMB, EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; 
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WMCGGRMEDIPCS -> SQLSRRPVLGTAS (in

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VARSPLIC

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STEALURESE FROWN N. TISSUE=Brain, and Breast tumor;
STRAIN-C57BL/6, and FVB/N; TISSUE=Brain, and Breast tumor;
REAUSDERGE FROWN N. Feingold E. A., Grouse L. H., Derge J. G.,
REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R. L., Feingold E. A., Grouse L. H., Derge J. G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.W.,
RA Hohron D.K., Muxny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Haltalon D.K., Muxny D.M., Madan A., Rodrigues S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz N., Marra M.A.,
RA Rodriguez A.C., Grimwood J., Schmutz N., Marra M.A.,
RA Schnerch A. Schein J.E., Jones S.J.M., Marra M.A.,
RT Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.",
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ON CHORGES

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OLI-OCT-2004 (Teal 45, Last enquence update)

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OLI-OCT-2004 (Teal 45, Last enquence update)

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SETRAIN=CS7BL/6J; TISSUB=Colon;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

Mikaido I., Coato M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Coato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D. P., Bult C., Hume D.A., Quackenbush J.,

Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Blake U.A., Bradt D., Brusic V., Chothia C., Corbail L.E., Cousins S.,

Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
                                                                                                                                                                             Gaps
                                                                                                                                                                             1;
                                                                                        93.8%; Score 217.5; DB 1; Length 603; 95.3%; Pred. No. 3.6e-21; Live 1; Mismatches 0; Indels 1;
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Best Local Similarity 95.20,
A1, Conservative
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RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kirochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magalott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.
RA Magabima T., Numata K., Okido T., Pavan W.J., Perrea G., Pescle G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Wilming L.G., Waynshaw-Boris A., Varnagisawa M., Yang I., Yang L.,
Wilming L.G., Wynshaw-Boris A., Varninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamuz M., Sakazume N., Saco,
RA Rasuishi A., Yoshino M., Aizawa K., Arakawa T., Fukuda S.,
Rhizaki T., Waki K., Sasaki D., Shibata K., Shinagawa A.,
Rayazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Ranalysis of the mouse transcriptome based on functional annotation of
M. Nature 420:563-573(2002).
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WE TISSUE SPECIFICITY.

MEDLINE=21264503; PubMed=11278534; DOI=10.1074/jbc.M009638200;

MEDLINE=21264503; PubMed=11278534; DOI=10.1074/jbc.M009638200;

The Hagen K.G., Bedi G.S., Tetaert D., Kingsley P.D., Hagen F.K.,

Balys M.M., Beres T.M., Degand P., Tabak L.A.;

Cloning and characterization of a ninth member of the UDP-

AGINAC.POPLYPEDTIGE N-acety1galactosaminyltransferase family,

D. Biol. Chem. 276:17395-17404 (2001).

U. Biol. Chem. 276:17395-17404 (2001).

C. I. FUNCTION: Catalyzes the initial reaction in O-linked

Oligosaccharide biosynthesis, the transfer of an N-acety1-D-

Galactosamine residue to a serine or threonine residue on the

protein receptor. Has activity toward MucSAc and EA2 peptide

C. CATALYTIC ACTIVITY: UDP-N-acety1-D-galactosamine + polypeptide =

C. CATALYTIC ACTIVITY: UDP-N-acety1-D-galactosamine + polypeptide =

C. CATALYTIC ACTIVITY: UDP-N-acety1-D-galactosamine + polypeptide =

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C. CATALYTIC ACTIVITY: UDP-N-acety1-D-galactosamine + polypeptide 
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SANIARATY: Contains 1 ricin B-type lectin domain.

CAUTION: According to experiments made in rat, this enzyme is unable to transfer GalNAc onto serine or threonine residue on the protein receptor, but instead requires the prior addition of a GalNAc on a peptide before adding additional GalNAc moietles, thereby acting as a glycopeptide transferase.
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Fri Nov 12 14:55:15 2004

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UDP + N-acetyl-D-galactosaminyl-polypeptide.
--- COFACTOR: Mangaes and calcium (By similarity).
--- PATHMAY: Glycosylation.
--- PATHMAY: LOCATION: Type II membrane protein. Golgi (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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   à
            RMEL; BC060617; AAH60617.1; A.M. RMEL; BC060617; AAH60617.1; -...
R RMEL; BC060617; AAH60617.1; -...
R RASB; P26514; LKOM.
R RSP; P26514; LKOM.
R RO; GO:0004653; P:polypeptide N-acetylgalactosaminyltransfera. . .; IDA.
GO; GO:0004653; F:polypeptide N-acetylgalactosaminyltransfera. . .; IDA.
GO; GO:0004653; F:polypeptide N-acetylgalactosaminyltransfera. . .; IDA.
R GO; GO:0004653; F:polypeptide N-acetylgalactosaminyltransfera. . .; IDA.
R GO; GO:0004653; F:polypeptide N-acetylgalactosaminyltransfera. . .; IDA.
R InterPro; IPR00173; Glycoctrans.
R InterPro; IPR00173; Glycoctrans.
R Ffam; PF00653; Glycoctrans.
R Ffam; PF00653; Ricin B lectin, 2.
R PROSSTER; RSC021; RICIN B LECTIN; 1.
R PROSSTER; RSC021; RICIN B LECTIN; 1.
Calcium; Glycosyltransferase; Transmembrane.
Cytoplasmic (Potential).
Cytoplasmic (Potential).
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Eukaryota, Metazca, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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-!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + polypeptide =
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By similarity.
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Nollinked (GlorAc. ...) (Potential).
Nollinked (GlorAc. ...) (Potential).
Nollinked (GlorAc. ...) (Potential).
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-!- FUNCTION: Catalyzes the initial reaction in O-linked oil oil osancharide losynthesis, the transfer of an N-acetyl-D-galactosamine residue to a serine or threonine residue on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., ENZYME ACTIVITY, AND TISSUE SPECIFICITY.
TISSUE-Sublingual gland;
MEDLINE-21264603; Pubmed-11278534; DOI=10.1074/jbc.M009638200;
Ten Hagen K.G., Bedi G.S., Tereart D., Kingsley P.D., Hagen F.K., Balys M.M., Beres T.M., Degand P., Tabak L.A.;
"Cloning and characterization of a ninth member of the UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase family, ppGaNTase-T9.";
J. Biol. Chem. 276:17395-17404(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic (Potential).
Signal-anchor for type II membrane protein (Potential).
Lumenal (Potential).
Catalytic subdomain A.
Catalytic subdomain B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 93.8%; Score 217.5; DB 1; Length 603; l Similarity 95.3%; Pred. No. 3.6e-21; 41; Conservative 1; Mismatches 0; Indels 1;
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   EMBL; BC016585; AAH16585.1; ALT_INIT
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                                                                                                                                                                                                                                                                                     -I- DOWAIN: There are two conserved domains in the glycosyltransferase region: the N-terminal domain (domain A, also called GT1 motif), which is probably involved in manganese coordination and substrate binding and the C-terminal domain (domain B, also called Gal/GalNAc-T motif), which is probably involved in catalytic reaction and UDP-Gal binding (By similarity).
-!- DOMAIN: The ricin B-type lectin domain binds to GalNAc and contributes to the glycospeptide specificity (By similarity).
-!- SIMILARITY: Belongs to the glycosyltransferase family 2. GalNAc-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 ricin B-type lectin domain.
-!- CAUTION: According Ref. 1, this enzyme is unable to transfer GalNAc onto serine or threonine residue on the protein receptor, but instead requires the prior addition of a GalNAc on a peptide before adding additional GalNAc moieties, thereby acting as a
similarity).
-!- TISSUE SPECIFICITY: Highly expressed in the sublingual gland,
testis, small intestine, colon and ovary. Expressed at
intermediate level in heart, brain, spleen, lung, stomach, cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal-anchor; Transferase; Transmembrane.

T DOMAIN

T RANSMEM

T PRANSMEM

T PRANSMEM

T CYtoplasmic (Potential).

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CAUTION: Was originally (Ref.1) termed Galnt9/pp-GaNTase 9.
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HSSP; P26614; 1KNL.
RGD; 69409; Galntio.
RIDERPRO; IPRO0173; Glyco trans_2.
InterPro; IPR008997; RicinB like.
InterPro; IPR00772; RicinB lectin.
Pfam; PF00525; RicinB lectin.
Pfam; PF00525; RicinB lectin.
Pfam; PF00552; RicinB Lectin.
PFAM; SMOAFS; RICIN B LECTIN; 1.
Calcium; Glycosyltransferase; Golgi stack; Lectin; Manganese;
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Best Local Similarity 95,3%
Thes 41; Conservative
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603 AA;
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STRAIN=PEST;
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01-MAR-2004
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Best Local
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Q7Q0E9
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Q7PZMS
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STRAIN=C57BL/6; TISSUB=Brain;

MEDLINE=22388257; PubMed=1247932;

MEDLINE=22388257; PubMed=1247932;

MEDLINE=22388257; PubMed=1247932;

MASTAIN=C57BL/6; Feingold B.A., Grouse L.H., Derge J.G.,

MISCAINI S.P., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

MASTACHI S.P., Jozdan H., Moore T., Max S.T., Wang J., Habte F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Michards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Mananan A., Maran M.A.,

Mananan A., Moores M.M., Sodergren E.D., Schnerch A., Schein J.E.,

Mananan A., Moores M.M., Schalska U., Smailus D.E., Schnerch A., Schein J.E.,

Mananan A., Manan M., Manan M., Manan M., Schner E.D., Dickson M.C.,

Mananan A., Maran M.A.,

Mananan A., Manan M., Schalska U., Smailus D.E., Schnerch A., Schein J.E.,

Mananan A., Manan M., Manan M., Manan M., Manan M., Schein J.E.,

Mananan M., Manan M., Manan M., Manan M., Schner E.D., Schner E.D., Schner E.D., Schner E.D., Marra M.A.,

Mananan M., Manan M., Manan M., Manan M., Schner E.D., Schner E.D., Marra M.A.,

Mananan M., Manan M., Manan M., Manan M., Schner E.D., Marra M.A.,

Mananan M., Manan M., Manan M., Manan M., Schner E.D., Marra M., Manan 
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Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
Kizamura H., Nakagawa T., Nagase T., Ohara, O., Koga H.;
Sagal Y., Kitamura H., Okaing Sequences of Mouse Homologues of Flu Gene
"Prediction of the Coding Sequences of Mouse Homologues of Flu Gene
The Complete Nucleotide Sequences of 110 Mouse Flu-homologous CDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ή,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAEVWM 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Strausberg R.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC060617; AAH60617.1; -.
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           12-MAY-2004 (TrEMBLrel. 27, Created)
12-MAY-2004 (TrEMBLrel. 27, Last sequence update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
UDP-N-acetyl-alpha-D-galactosamine:polypeptide
GALNTIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2004 (TrEMBLrel. 27, Created)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
MFLJ00205 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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   603 AA
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STRAIN=C57BL/6; TISSUE=Brain;
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nes 41; Conservative
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       PRELIMINARY;
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Identified by Screening of Terminal sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AK131155; BAD21405.1; -.
NOW TER 1
SEQUENCE 634 AA; 72315 MW; C79B82D4D0052C81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Name=agCG54007; ORFNames=ENSANGG00000009226;
Anopheles gambiae str. PEST.
Bucheles gambiae str. PEST.
Bucheles gambiae str. Pest.
Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=agCG54449; ORFNames=ENSANGG0000012813;
Name=agCG5449; ORFNames=ENSANGG0000012813;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoldea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles Genome Sequencing Consortium;
Anopheles Genome Sequencing Consortium;
Submitted (MAK-2002) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Local Similarity 61.4%; Pred. No. 7.4e-11;
nes 27; Conservative 6; Mismatches 9; Indels
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                                                                                                                                                                                                              93.8%; Score 217.5; DB 2; Length 95.3%; Pred. No. 3.8e-21; ive __1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anotheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          387 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLARNLKRVAEVWM 429
                                                                                                                                                                                                                                                                                                                                       42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  599 AA; 69224 MW; DA646C182B143028 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     599 AA
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EMBL; AAABO1008986; EAA00339.1; -.

InterPro; IPR000173; Glyco_trans_2.

InterPro; IPR00072; Ricin_Blectin.

Pfam; PF00535; Glycos_transf_2; 1.

Pfam; PF00525; Ricin_Blectin; 3.

PROSITE; PS50231; RICIN_BLECTIN; 1.

NOW TER 1

SEQUENCE 599 AA; 69224 MW; DA646C18
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                                                                                                                                                                                                                                                                                 41; Conservative
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Fri Nov 12 14:55:15 2004

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RESULT 9

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galactosamine residue to a serine or threonine residue on the
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Astachench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M. J. Usdin T.B., Toobhlyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toobhlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton B., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bonffard G.G.,
Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M.,
Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,
Goneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTLL HUMAN STANDARD; PRT; 558 AA.

GM428; Q9ULT9;

Q8N428; Q9ULT9;

Q1-CT-2004 (Rel. 45, Last sequence update)

O1-CCT-2004 (Rel. 45, Last annotation update)

O1-CCT-2004 (Rel. 45, Last annotation update)

Putative polypeptide Nacetylgalactosaminyltransferase-like protein 1)

Putative polypeptide Nacetylgalactosaminyltransferase-like protein 1) (UDP-GalNAc:pOlypeptide N-acetylgalactosaminyltransferase-like protein 1) (Polypeptide GalNAc transferase-like protein 1)

(GalNAC-T-like protein 1) (pp-GaNTase-like protein 1)

Name-GALNTL1; Synonyms-KIAA1130;

Homo sapiens (Human)
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain."; DNA Res. 6:329-336(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                            5,
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MEDIINE=20039618; PubMed=10574461;
Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
                                                                                                                                                                                                                                                Length 644;
                                                                                                                                                                                                                                            Query Match 56.5%; Score 131; DB 2; Length 64 Best Local Similarity 61.4%; Pred. No. 3.6e-09; Matches 27; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                      CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS-LARNLKRVAD-WM 42
                                                                                                                                                                                                         644 AA; 74214 MW; 0B7AB007BC228501 CRC64;
                                       Preliminary data.

EMBL; AAAB01008986; EAA00190.1; -.
InterPro; IPR000173; Glyco_trans_2.
InterPro; IPR000772; Ricin_Blectin.
Pfam; PF00535; Glycos_transf_2; 1.
Pfam; PF00525; Ricin_Blectin; 3.
PROSITE; PS50231; RICIN_B_LECTIN; 1.
NON_TER 1 1 1 1 1 1 SEQUENCE 644 AA; 74214 MW; 0B7AB007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Cytoplasmic (rot type II membrane protein (Potential).

Lumenal (Potential).

Catalytic subdomain A.

Catalytic subdomain B.

Richi B-rype lectin.

By similarity.

By similarity.

By similarity.

KWRRKGSFPQHSVGULETKPAQLVTSKCQADAQAQWQL

LPHT -> VGLLASGPEAQQPEGPCLRVADLGRRAPD (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note-No experimental confirmation available;

Note-No experimental confirmation available;

-1-DOMAIN: There are two conserved domains in the glycosyltransferase region: the N-terminal domain (domain A, also called GT1 motif), which is probably involved in marganese coordination and substrate binding and the C-terminal domain (domain B, also called Gal/GalNac-T motif), which is probably involved in catalytic reaction and UDP-Gal binding (By similarity).

-1-DOMAIN: The ricin B-type lectin domain binds to GalNAc and contributes to the glycopeptide specificity (By similarity).

-1-SIMILARITY: Belongs to the glycosyltransferase family 2. GalNAc-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
protein receptor (By similarity).
CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50231; RICIN B LECTIN; 1.
Alternative splicing; Calcium; Glycosyltransferase; Golgi stack; Lectin; Manganese; Signal-anchor; Transferase; Transmembrane.
DOMAIN
Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
m
                                                                UDP + Nacetyl-D-galactosaminyl-polypeptide.
-!- COFACTOR: Manganese and calcium (By similarity).
-!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.4%; Score 128.5; DB 1; Length 558; Best Local Similarity 55.6%; Pred. No. 6.9e-09; Matches 25; Conservative 6; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 CGGSLEIVPCSRVGHVFRKRHPYNFPEGNALTYIRNTKRTAEVWM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLA--RNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARIÎY: Contains 1 ricin B-type lectin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoform 2).
/FTIG=VSP 011231.
558 AA; 63074 MW; FP35C5606B5291B8 CRC64;
                                                                                                                                                                                                                                 similarity).
-!- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing, Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               [soId=Q8N428-2; Sequence=VSP_011231;
                                                                                                                                                                                                                                                                                                                                                                                  IsoId=08N428-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB032956; BAA86444.1; ALT_INIT.
EMBL; BC036812; AA436812.1; ALT_INIT.
Genew; HGNC:2323; GALNILL.
INTERPRO; IPR001173; GIVOC trans 2.
INTERPRO; IPR008997; RicinB like.
InterPro; IPR000772; RicinB lectin.
Pfam; PF00535; GIYCOS transf2; 1.
Pfam; PF00552; RicinB lectin.
SMART; SM00458; RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56
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